



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 95546

TO: Jeffrey Parkin  
Location: CM1 8E15  
Art Unit: 1648  
Thursday, June 05, 2003

Case Serial Number: 605573

From: Alex Waclawiw  
Location: Biotech-Chem Library  
CM1-6A02  
Phone: 308-4491

Alexandra.waclawiw@uspto.gov

### Search Notes

Examiner Parkin,

I was not able to remove the inventor's name from the compugen search. The program does not allow for that option.

I also searched the sequence on STN. There were no sequences with less than 20 amino acids. I printed out hits with sequence length between 20-30 amino acids just in case this information would be useful. The reference for these sequences was the inventor's work

Alexandra Waclawiw

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# STIC SEARCH RESULTS FEEDBACK FORM

## Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher* or contact:

Mary Hale, Information Branch Supervisor  
308-4258, CM1-1E01

## Voluntary Results Feedback Form

➤ I am an examiner in Workgroup:  Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature  
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC/Biotech-Chem Library CM1 - Circ. Desk



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Parkin 09/605,573

=>adhis

(FILE 'HOME' ENTERED AT 10:54:21 ON 05 JUN 2003)

FILE 'REGISTRY' ENTERED AT 10:55:14 ON 05 JUN 2003

L1 16 S LNSWGCKGRIICYTS/SQSP  
L2 0 S L1 AND SQL<21  
L3 0 S L1 AND SQL=20  
L4 9 S L1 AND SQL<31

FILE 'HCAPLUS' ENTERED AT 10:58:23 ON 05 JUN 2003  
L5 1 S L4

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=> fil reg

FILE 'REGISTRY' ENTERED AT 10:58:51 ON 05 JUN 2003  
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.  
PLEASE SEE "HELP USAGETERMS" FOR DETAILS.  
COPYRIGHT (C) 2003 American Chemical Society (ACS)

Property values tagged with IC are from the ZIC/VINITI data file  
provided by InfoChem.

STRUCTURE FILE UPDATES: 4 JUN 2003 HIGHEST RN 525536-93-0  
DICTIONARY FILE UPDATES: 4 JUN 2003 HIGHEST RN 525536-93-0

TSCA INFORMATION NOW CURRENT THROUGH JANUARY 6, 2003

Please note that search-term pricing does apply when  
conducting SmartSELECT searches.

Crossover limits have been increased. See HELP CROSSOVER for details.

Experimental and calculated property data are now available. See HELP  
PROPERTIES for more information. See STNnote 27, Searching Properties  
in the CAS Registry File, for complete details:  
<http://www.cas.org/ONLINE/STN/STNOTES/stnotes27.pdf>

=> d que 14

L1 16 SEA FILE=REGISTRY ABB=ON PLU=ON LNSWGCKGRIICYTS/SQSP  
L4 9 SEA FILE=REGISTRY ABB=ON PLU=ON L1 AND SQL<31

=> d sqide3 14 1-9

L4 ANSWER 1 OF 9 REGISTRY COPYRIGHT 2003 ACS  
RN 276694-91-8 REGISTRY  
CN L-Histidine, glycy-L-arginyl-L-.alpha.-glutamyl-L-threonyl-L-leucyl-L-  
methionyl-L-glutaminyglycyl-L-glutaminyl-L-glutaminyl-L-phenylalanyl-L-  
leucyl-L-asparaginy-L-seryl-L-tryptophylglycyl-L-cysteinyl-L-lysylglycyl-  
L-arginyl-L-isoleucyl-L-isoleucyl-L-cysteinyl-L-tyrosyl-L-threonyl-L-seryl-  
L-alanyl-L-arginyl-L-tryptophyl- (9CI) (CA INDEX NAME)  
OTHER NAMES:  
CN 4: PN: JP2000157268 PAGE: 37 claimed sequence  
FS PROTEIN SEQUENCE; STEREOSEARCH  
SQL 30

PATENT ANNOTATIONS (PNTE):

Sequence	Patent
Source	Reference
Not Given	JP2000157268
	claimed PAGE
	37

SEQ3 1 Gly-Arg-Glu-Thr-Leu-Met-Gln-Gly-Gln-Gln-  
11 Phe-Leu-Asn-Ser-Trp-Gly-Cys-Lys-Gly-Arg-  
===  
21 Ile-Ile-Cys-Tyr-Thr-Ser-Ala-Arg-Trp-His  
===

HITS AT: 12-26

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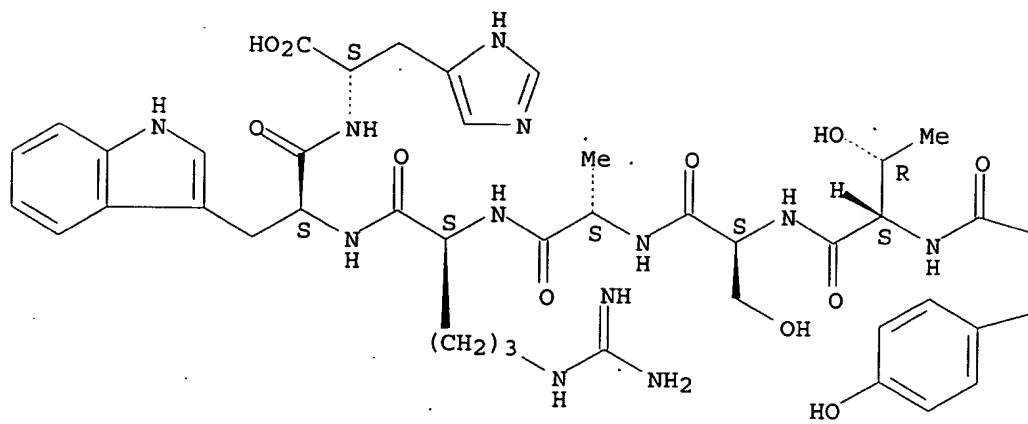
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SR      CA

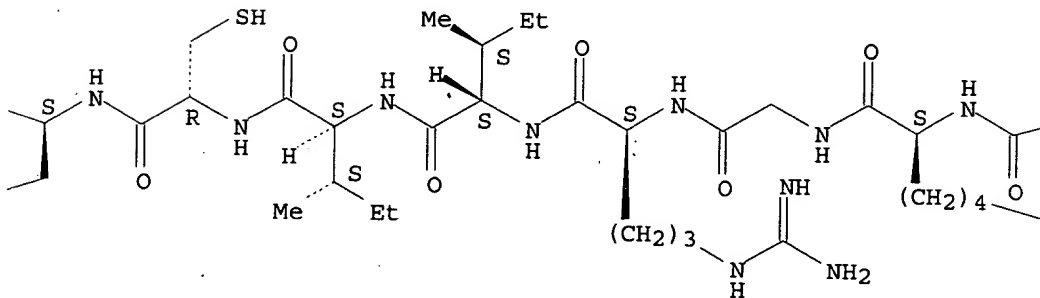
LC STN Files: CA, CAPLUS, USPATFULL

Absolute stereochemistry.

PAGE 1-A

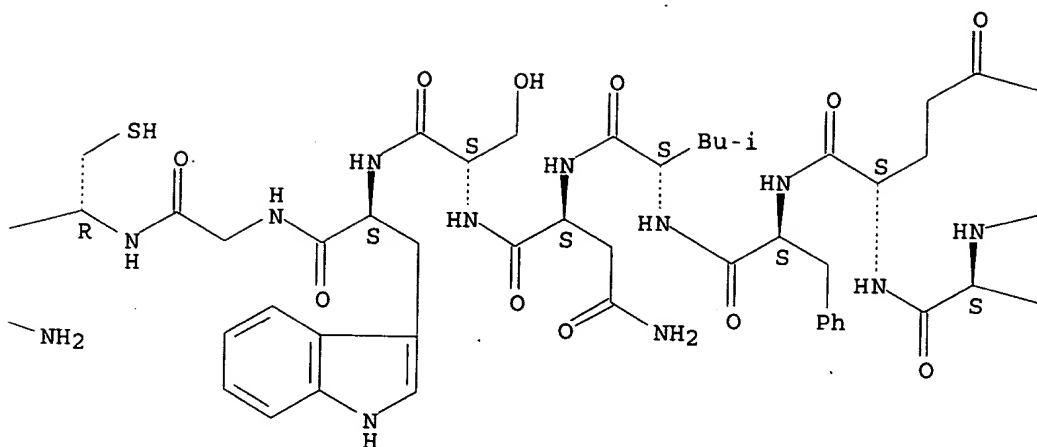


PAGE 1-B

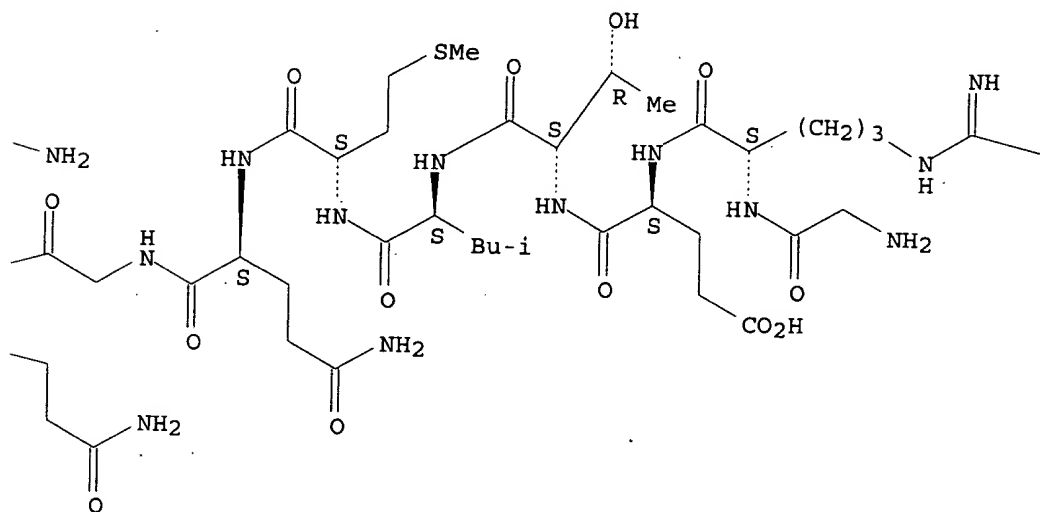


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PAGE 1-C



PAGE 1-D



PAGE 1-E

NH<sub>2</sub>

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1 REFERENCES IN FILE CA (1957 TO DATE)  
 1 REFERENCES IN FILE CAPLUS (1957 TO DATE)

L4 ANSWER 2 OF 9 REGISTRY COPYRIGHT 2003 ACS  
 RN 276687-01-5 REGISTRY  
 CN Peptide, (Glu-Thr-Leu-Met-Gln-Xaa-Gln-Gln-Arg-Leu-Asn-Ser-Trp-Gly-Cys-Lys-  
 Gly-Arg-Ile-Ile-Cys-Tyr-Thr-Ser-Ala-Arg-Trp-His) (9CI) (CA INDEX NAME)  
 OTHER NAMES:  
 CN 6: PN: JP2000157268 PAGE: 37 claimed sequence  
 FS PROTEIN SEQUENCE  
 SQL 28  
 NTE

type	location	description
uncommon	Aaa-6	

## PATENT ANNOTATIONS (PNTE):

Sequence	Patent
Source	Reference
Not Given	JP2000157268 claimed PAGE 37

SEQ3 1 Glu-Thr-Leu-Met-Gln-Aaa-Gln-Gln-Arg-Leu-  
 11 Asn-Ser-Trp-Gly-Cys-Lys-Gly-Arg-Ile-Ile-  
 21 Cys-Tyr-Thr-Ser-Ala-Arg-Trp-His

HITS AT: 10-24

## \*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

MF Unspecified  
 CI MAN  
 SR CA  
 LC STN Files: CA, CAPLUS, USPATFULL  
 1 REFERENCES IN FILE CA (1957 TO DATE)  
 1 REFERENCES IN FILE CAPLUS (1957 TO DATE)

L4 ANSWER 3 OF 9 REGISTRY COPYRIGHT 2003 ACS  
 RN 276687-00-4 REGISTRY  
 CN Peptide, (Xaa-Gln-Gln-Arg-Leu-Asn-Ser-Trp-Gly-Cys-Lys-Gly-Arg-Ile-Ile-Cys-  
 Tyr-Thr-Ser-Ala-Arg-Trp-His) (9CI) (CA INDEX NAME)  
 OTHER NAMES:  
 CN 5: PN: JP2000157268 PAGE: 37 claimed sequence  
 FS PROTEIN SEQUENCE  
 SQL 23  
 NTE

type	location	description
uncommon	Aaa-1	

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PATENT ANNOTATIONS (PNTE):

Sequence	Patent
Source	Reference
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Not Given	JP2000157268
	claimed PAGE
	37

SEQ3 1 Aaa-Gln-Gln-Arg-Leu-Asn-Ser-Trp-Gly-Cys-  
 11 Lys-Gly-Arg-Ile-Ile-Cys-Tyr-Thr-Ser-Ala-  
 21 Arg-Trp-His  
 HITS AT: 5-19

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

MF Unspecified  
 CI MAN  
 SR CA  
 LC STN Files: CA, CAPLUS, USPATFULL  
 1 REFERENCES IN FILE CA (1957 TO DATE)  
 1 REFERENCES IN FILE CAPLUS (1957 TO DATE)  
 L4 ANSWER 4 OF 9 REGISTRY COPYRIGHT 2003 ACS  
 RN 276250-49-8 REGISTRY  
 CN 4: PN: JP2000157268 SEQID: 63 unclaimed protein (9CI) (CA INDEX NAME)  
 FS PROTEIN SEQUENCE  
 SQL 30  
 NTE

type	location	description
uncommon	Aaa-8	

PATENT ANNOTATIONS (PNTE):

Sequence	Patent
Source	Reference
=====	
Not Given	JP2000157268
	unclaimed
	SEQID 63

SEQ3 1 Gly-Arg-Glu-Thr-Leu-Met-Gln-Aaa-Gln-Gln-  
 11 Arg-Leu-Asn-Ser-Trp-Gly-Cys-Lys-Gly-Arg-  
 21 Ile-Ile-Cys-Tyr-Thr-Ser-Ala-Arg-Trp-His  
 HITS AT: 12-26

MF Unspecified  
 CI MAN  
 SR CA  
 LC STN Files: CA, CAPLUS, USPATFULL  
 1 REFERENCES IN FILE CA (1957 TO DATE)  
 1 REFERENCES IN FILE CAPLUS (1957 TO DATE)

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L4 ANSWER 5 OF 9 REGISTRY COPYRIGHT 2003 ACS  
 RN 276250-48-7 REGISTRY  
 CN 3: PN: JP2000157268 SEQID: 62 unclaimed protein (9CI) (CA INDEX NAME)  
 FS PROTEIN SEQUENCE  
 SQL 28  
 NTE

type	location	description
uncommon	Aaa-6	

## PATENT ANNOTATIONS (PNTE):

Sequence	Patent
Source	Reference
Not Given	JP2000157268
	unclaimed
	SEQID 62

SEQ3 1 Glu-Thr-Leu-Met-Gln-Aaa-Gln-Gln-Arg-Leu-  
 11 Asn-Ser-Trp-Gly-Cys-Lys-Gly-Arg-Ile-Ile-  
 21 Cys-Tyr-Thr-Ser-Ala-Arg-Trp-His

HITS AT: 10-24

## \*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

MF Unspecified  
 CI MAN  
 SR CA  
 LC STN Files: CA, CAPLUS, USPATFULL  
 1 REFERENCES IN FILE CA (1957 TO DATE)  
 1 REFERENCES IN FILE CAPLUS (1957 TO DATE)

L4 ANSWER 6 OF 9 REGISTRY COPYRIGHT 2003 ACS  
 RN 276250-47-6 REGISTRY  
 CN 2: PN: JP2000157268 SEQID: 60 unclaimed protein (9CI) (CA INDEX NAME)  
 FS PROTEIN SEQUENCE  
 SQL 23  
 NTE

type	location	description
uncommon	Aaa-1	

## PATENT ANNOTATIONS (PNTE):

Sequence	Patent
Source	Reference
Not Given	JP2000157268
	unclaimed
	SEQID 60

SEQ3 1 Aaa-Gln-Gln-Arg-Leu-Asn-Ser-Trp-Gly-Cys-

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=====
11 Lys-Gly-Arg-Ile-Ile-Cys-Tyr-Thr-Ser-Ala-
=====

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21 Arg-Trp-His

HITS AT: 5-19

\*\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*\*

MF Unspecified

CI MAN

SR      CA

LC STN Files: CA, CAPLUS, USPATFULL

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L4 ANSWER 7 OF 9 REGISTRY COPYRIGHT 2003 ACS

RN 275801-53-1 REGISTRY

CN 135: PN: JP2000157268 SEQID: 69 unclaimed sequence (9CI) (CA INDEX NAME)  
 ES PROTEIN SEQUENCE: STREPTOCOCCUS

FS PROTEIN SEQUENCE; STEREOSEARCH

SQL 30

## PATENT ANNOTATIONS (PNTE) :

Sequence	Patent
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Source	Reference
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=====+=====

Not Given|JP2000157268

01200019,	unclaimed
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SEQID 69

SEQ3 1 Gly-Arg-Glu-Thr-Leu-Met-Gln-Asp-Gln-Gln-

11 Arg-Leu-Asn-Ser-Trp-Gly-Cys-Lys-Gly-Arg-

	f	m	syl	lys	cry	arg	
==	==	==	==	==	==	==	==

21 Ile-Ile-Cys-Tyr-Thr-Ser-Ala-Arg-Trp-His

=====

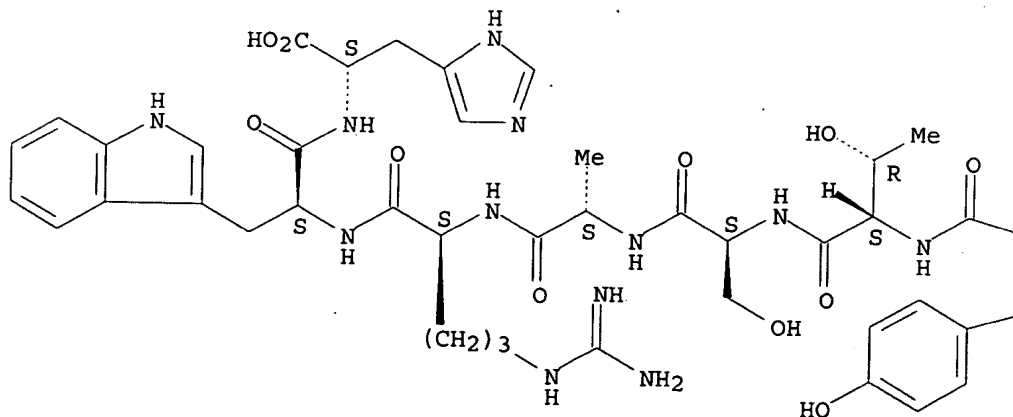
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SR      CA

LC STN Files: CA, CAPLUS, USPATFULL

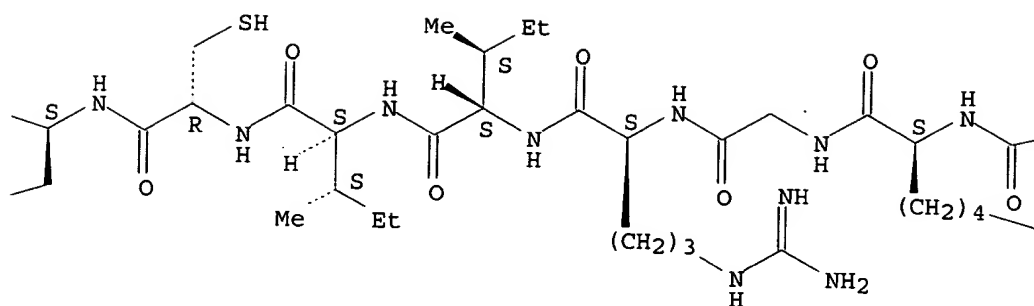
Absolute stereochemistry.



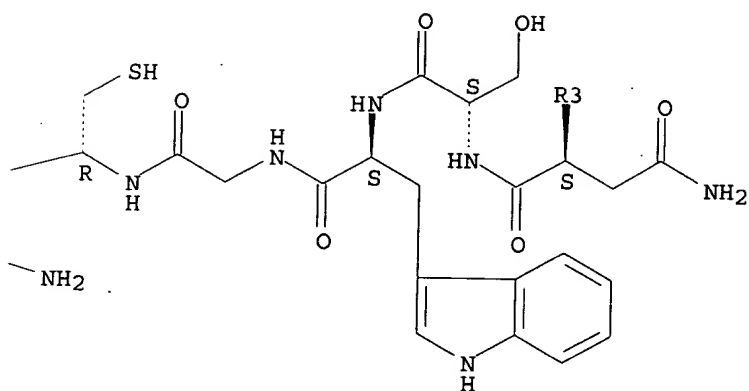
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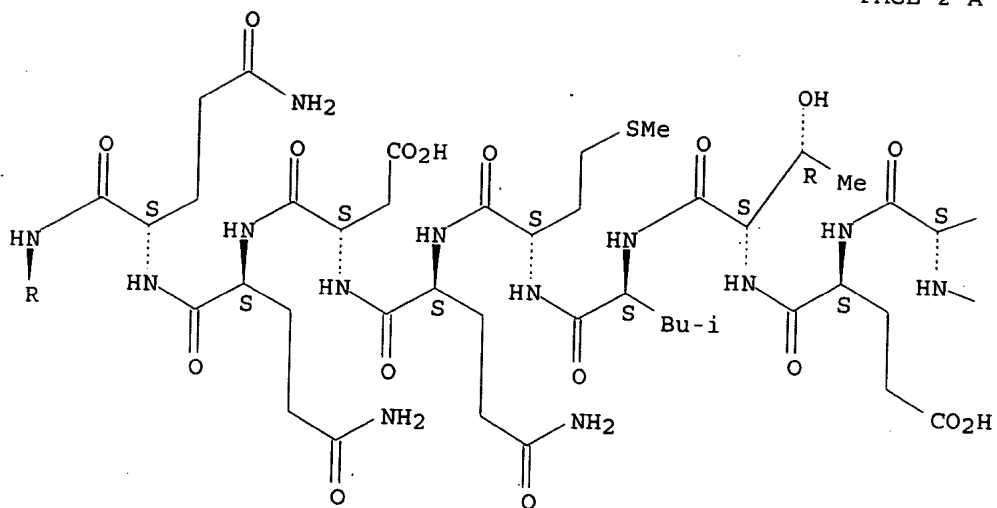


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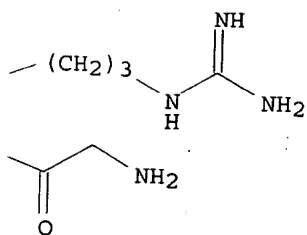


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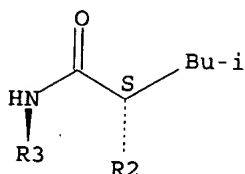
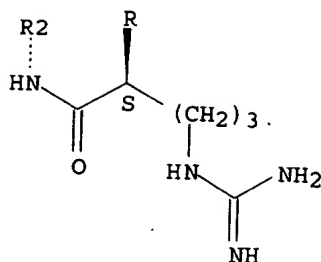
PAGE 2-A



PAGE 2-B



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1 REFERENCES IN FILE CA (1957 TO DATE)  
1 REFERENCES IN FILE CAPLUS (1957 TO DATE)

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RN 275801-51-9 REGISTRY  
CN L-Histidine, L-.alpha.-glutamyl-L-glutaminyl-L-glutaminyl-L-arginyl-L-leucyl-L-asparaginyl-L-seryl-L-tryptophylglycyl-L-cysteinyl-L-lysylglycyl-L-arginyl-L-isoleucyl-L-isoleucyl-L-cysteinyl-L-tyrosyl-L-threonyl-L-seryl-L-alanyl-L-arginyl-L-tryptophyl- (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 127: PN: JP2000157268 SEQID: 61 unclaimed sequence  
FS PROTEIN SEQUENCE; STEREOSEARCH  
SQL 23

PATENT ANNOTATIONS (PNTE):

Sequence	Patent
Source	Reference
Not Given	JP2000157268
	unclaimed
	SEQID 61

SEQ3 1 Glu-Gln-Gln-Arg-Leu-Asn-Ser-Trp-Gly-Cys-  
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11 Lys-Gly-Arg-Ile-Ile-Cys-Tyr-Thr-Ser-Ala-  
=====  
21 Arg-Trp-His

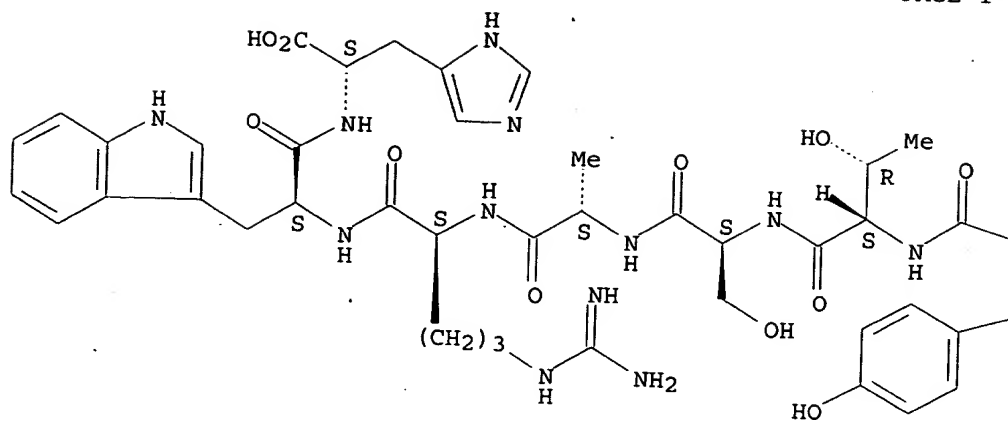
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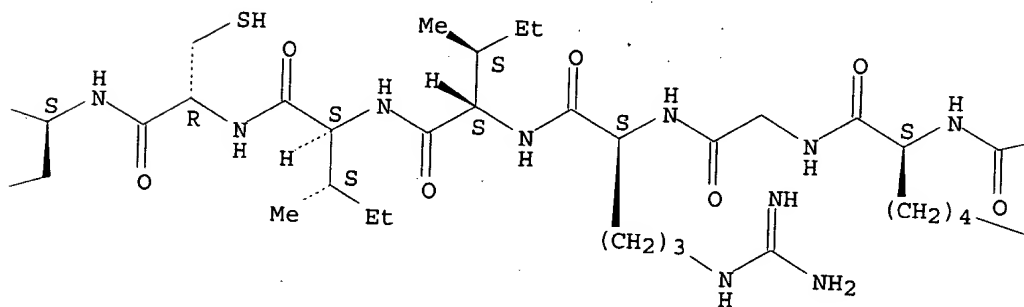
Absolute stereochemistry.

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PAGE 1-A

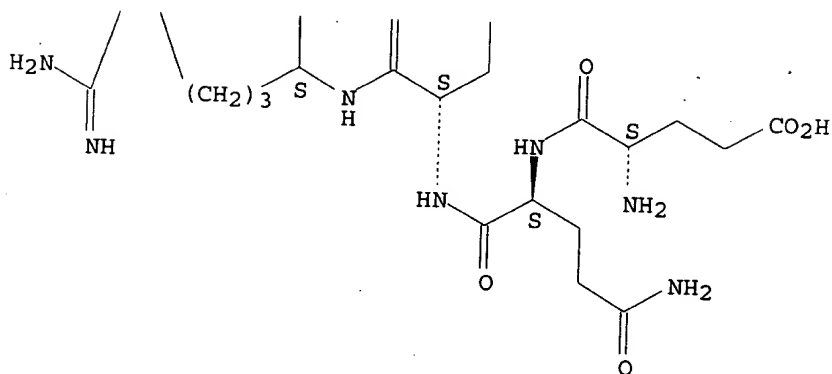
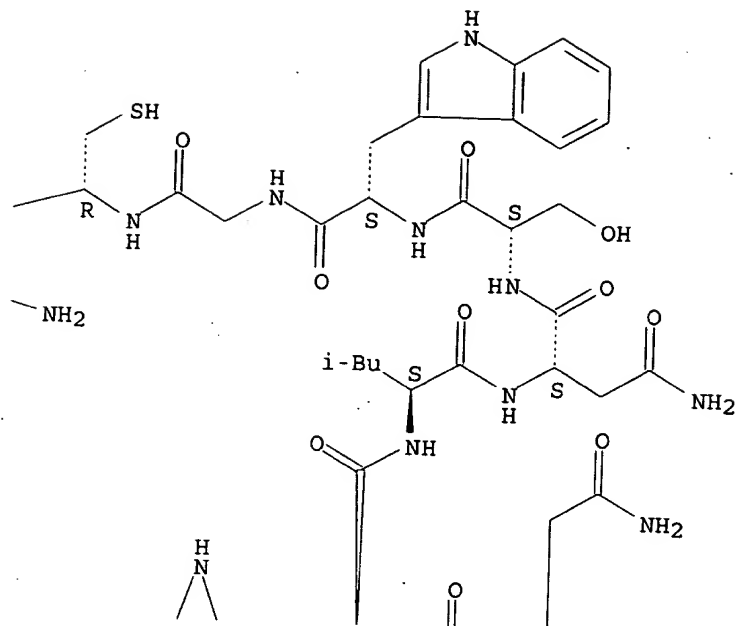


PAGE 1-B



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1 REFERENCES IN FILE CAPLUS (1957 TO DATE)

L4 ANSWER 9 OF 9 REGISTRY COPYRIGHT 2003 ACS  
RN 275801-47-3 REGISTRY  
CN L-Histidine, L-asparaginyl-L-glutaminyl-L-glutaminyl-L-arginyl-L-leucyl-L-asparaginyl-L-seryl-L-tryptophylglycyl-L-cysteinyll-L-lysylglycyl-L-arginyl-L-isoleucyl-L-isoleucyl-L-cysteinyll-L-tyrosyl-L-threonyll-L-seryl-L-alanyl-L-arginyl-L-tryptophyl- (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 125: PN: JP2000157268 SEQID: 59 unclaimed sequence  
FS PROTEIN SEQUENCE; STEREOSEARCH  
SQL 23

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PATENT ANNOTATIONS (PNTE):

Sequence	Patent
Source	Reference
Not Given	JP2000157268
	unclaimed
	SEQID 59

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SEQ3 1 Asn-Gln-Gln-Arg-Leu-Asn-Ser-Trp-Gly-Cys-

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21 Arg-Trp-His

HITS AT: 5-19

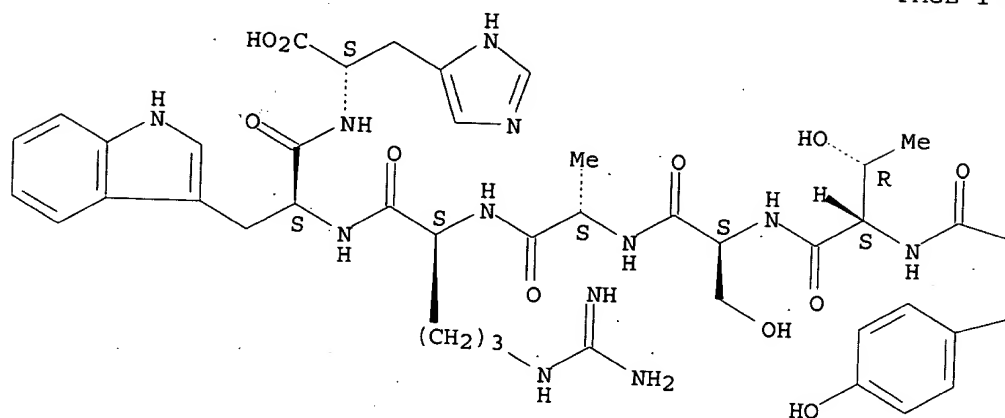
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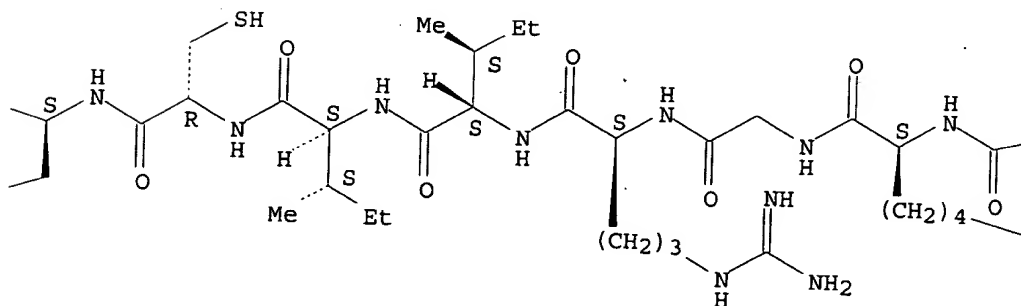
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Absolute stereochemistry.

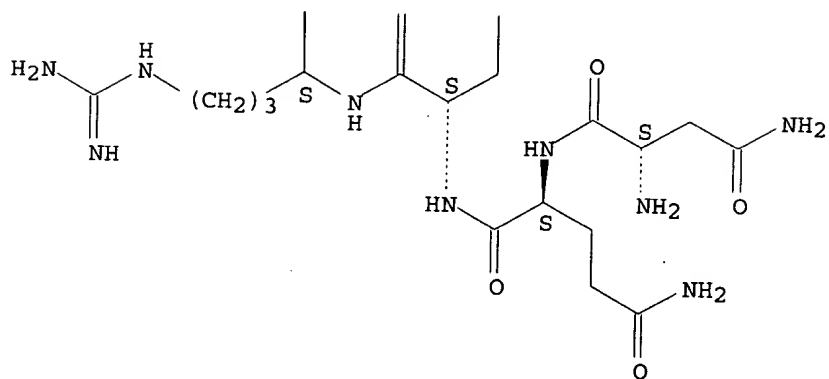
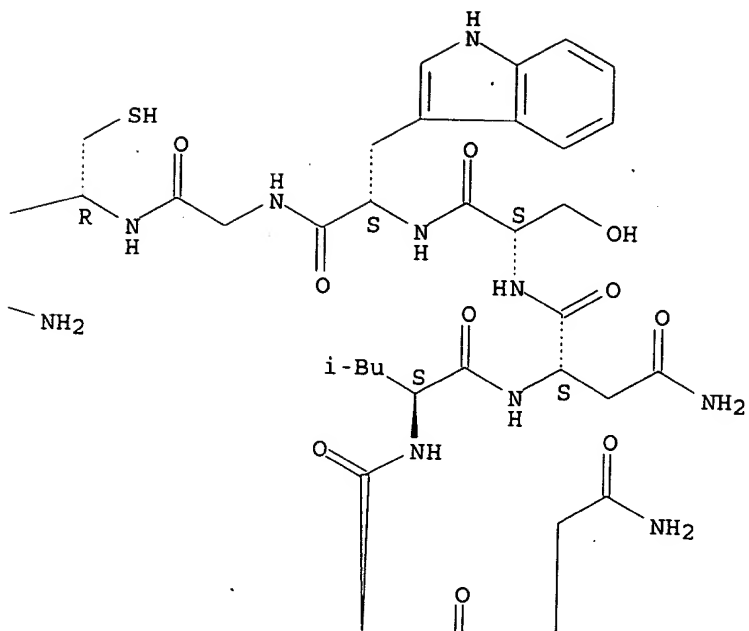
PAGE 1-A



PAGE 1-B



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1 REFERENCES IN FILE CA (1957 TO DATE)  
1 REFERENCES IN FILE CAPLUS (1957 TO DATE)

=> fil hcaplus

FILE 'HCAPLUS' ENTERED AT 10:59:08 ON 05 JUN 2003

USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.

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FILE COVERS 1907 - 5 Jun 2003 VOL 138 ISS 23  
FILE LAST UPDATED: 4 Jun 2003 (20030604/ED)

This file contains CAS Registry Numbers for easy and accurate substance identification.

'OBI' IS DEFAULT SEARCH FIELD FOR 'HCAPLUS' FILE

=> d que nos 15

L1 16 SEA FILE=REGISTRY ABB=ON PLU=ON LNSWGCKGRIICYTS/SQSP  
L4 9 SEA FILE=REGISTRY ABB=ON PLU=ON L1 AND SQL<31  
L5 1 SEA FILE=HCAPLUS ABB=ON PLU=ON L4

=> d .ca 15

L5 ANSWER 1 OF 1 HCAPLUS COPYRIGHT 2003 ACS  
ACCESSION NUMBER: 2000:392837 HCAPLUS  
DOCUMENT NUMBER: 133:55969  
TITLE: Peptide for detection of Group O HIV-1 and use for diagnosis  
INVENTOR(S): Deleys, Robert; Chen, Jan  
PATENT ASSIGNEE(S): Ortho-Clinical Diagnostics, Inc., USA  
SOURCE: Jpn. Kokai Tokkyo Koho, 103 pp.  
CODEN: JKXXAF  
DOCUMENT TYPE: Patent  
LANGUAGE: Japanese  
FAMILY ACC. NUM. COUNT: 1  
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
JP 2000157268	A2	20000613	JP 1999-338385	19991129
US 6149910	A	20001121	US 1999-433428	19991104
EP 1013766	A2	20000628	EP 1999-309491	19991129
EP 1013766	A3	20030129		

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO

PRIORITY APPLN. INFO.:

US 1998-110292P P 19981130  
US 1999-119138P P 19990208  
US 1999-433428 A 19991104

AB Disclosed are the peptides derived from the immunodominant region of the Group O HIV-1 gp41 envelope protein, which do not correspond to any known naturally occurring Group O sequence or variant. The peptides bind to the antibodies to Group O HIV-1. The peptides are useful in detecting antibodies arise from the infection by Group O HIV-1. The peptides may be prepd. in a hybrid form with that of Group M HIV-1.

IC ICM C12N015-00  
ICS C07K014-16; C07K016-12; C12N001-15; C12N001-19; C12N001-21; C12N005-10; C12P021-02; G01N033-569; C12P021-08

CC 10-1 (Microbial, Algal, and Fungal Biochemistry)

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Section cross-reference(s): 14  
 IT 276687-00-4 276687-01-5 276694-91-8  
 276873-37-1  
 RL: ARG (Analytical reagent use); BSU (Biological study, unclassified);  
 THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study);  
 USES (Uses)  
 (antibody to Group O HIV-1 detection by; peptide for detection of Group  
 O HIV-1 and use for diagnosis)  
 IT 275389-20-3 275389-22-5 275829-31-7 276250-39-6 276250-40-9  
 276250-41-0 276250-42-1 276250-43-2 276250-47-6  
 276250-48-7 276250-49-8 276250-50-1 276873-73-5  
 RL: PRP (Properties)  
 (unclaimed protein sequence; peptide for detection of Group O HIV-1 and  
 use for diagnosis)  
 IT 173145-89-6 275389-13-4 275389-14-5 275389-15-6 275389-16-7  
 275389-17-8 275389-18-9 275389-19-0 275801-47-3  
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 276249-52-6 276249-53-7 276249-62-8 276249-72-0 276249-78-6  
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 276250-27-2 276250-28-3 276250-29-4 276250-30-7 276250-31-8  
 276250-32-9 276250-33-0 276250-34-1 276250-35-2 276250-36-3  
 276250-37-4  
 RL: PRP (Properties)  
 (unclaimed sequence; peptide for detection of Group O HIV-1 and use for  
 diagnosis)

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 5, 2003, 07:21:32 ; Search time 13 Seconds

(Without alignments)  
33.950 Million cell updates/sec

Title: US-09-605-573A-69\_COPY\_12\_26

Perfect score: .89

Sequence: 1 LNSWCGCKRITCYTS 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 136623

Minimum DB seq length: 0

Maximum DB seq length: 21

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents AA:\*

1: /cgn2\_6/prodata/1/1aa/5A.COMB.pep:\*

2: /cgn2\_6/prodata/1/1aa/5B.COMB.pep:\*

3: /cgn2\_6/prodata/1/1aa/6A.COMB.pep:\*

4: /cgn2\_6/prodata/1/1aa/6B.COMB.pep:\*

5: /cgn2\_6/prodata/1/1aa/PCITUS.COMB.pep:\*

6: /cgn2\_6/prodata/1/1aa/Backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	72	80.9	15	1	US-08-615-279-8
2	72	80.9	15	1	US-08-615-279-8
3	68	76.4	19	1	US-08-472-597A-4
4	68	76.4	19	1	US-08-837-732-4
5	63	70.8	19	1	US-08-472-597A-3
6	63	70.8	19	1	US-08-837-732-3
7	59	66.3	19	1	US-08-472-597A-2
8	59	66.3	19	1	US-08-837-732-2
9	56	62.9	14	4	US-08-682-791B-7
10	56	62.9	14	4	US-08-682-791B-8
11	55	61.8	16	1	US-08-682-791B-11
12	55	61.8	16	1	US-08-615-279-27
13	55	61.8	16	1	US-08-765-452-7
14	54	60.7	14	1	US-08-615-279-32
15	54	60.7	14	2	US-08-765-452-11
16	54	60.7	15	1	US-07-633-964-8
17	54	60.7	15	3	US-08-386-956-8
18	54	60.7	15	3	US-09-108-709-12
19	54	60.7	19	1	US-08-472-597A-1
20	54	60.7	19	1	US-08-837-732-1
21	53	59.6	12	2	US-08-146-028-5
22	53	59.6	12	4	US-08-723-425A-5
23	53	59.6	12	4	US-09-112-206-5
24	53	59.6	16	4	US-09-009-953-131
25	53	59.6	19	1	US-07-901-874B-14
26	53	59.6	19	1	US-08-457-865-14
27	53	59.6	20	1	US-07-633-964-14

28	53	59.6	20	1	US-08-386-956-14	Sequence 14, Appl
29	53	59.6	20	3	US-09-108-709-45	Sequence 45, Appl
30	53	59.6	21	2	US-08-146-028-2	Sequence 2, Appl1
31	53	59.6	21	4	US-08-723-425A-2	Sequence 2, Appl1
32	53	59.6	21	4	US-09-112-206-2	Sequence 2, Appl1
33	51	57.3	12	1	US-07-633-964-2	Sequence 2, Appl1
34	51	57.3	12	1	US-07-633-964-2	Sequence 2, Appl1
35	51	57.3	12	1	US-07-633-964-28	Sequence 28, Appl
36	51	57.3	12	1	US-07-633-964-29	Sequence 29, Appl
37	51	57.3	12	1	US-08-218-025A-121	Sequence 121, App
38	51	57.3	12	1	US-08-386-956-2	Sequence 2, Appl1
39	51	57.3	12	1	US-08-386-956-28	Sequence 28, Appl
40	51	57.3	12	1	US-08-386-956-29	Sequence 29, Appl
41	51	57.3	12	3	US-09-108-709-2	Sequence 2, Appl1
42	51	57.3	12	3	US-09-108-709-17	Sequence 17, Appl
43	51	57.3	12	3	US-08-776-949-27	Sequence 27, Appl
44	51	57.3	13	3	US-09-108-709-18	Sequence 18, Appl
45	51	57.3	13	3	US-09-108-709-19	Sequence 19, Appl
46	51	57.3	13	3	US-09-108-709-20	Sequence 20, Appl
47	50	56.2	12	1	US-07-633-964-4	Sequence 4, Appl1
48	50	56.2	12	1	US-08-386-956-4	Sequence 4, Appl1
49	50	56.2	12	3	US-09-108-709-25	Sequence 25, Appl
50	50	56.2	13	3	US-09-108-709-26	Sequence 26, Appl
51	50	56.2	13	3	US-09-108-709-27	Sequence 27, Appl
52	50	56.2	14	3	US-09-108-709-28	Sequence 28, Appl
53	50	56.2	14	4	US-08-682-791B-3	Sequence 3, Appl1
54	50	56.2	16	1	US-07-901-874B-16	Sequence 16, Appl
55	50	56.2	16	1	US-08-457-865-16	Sequence 16, Appl
56	50	56.2	18	6	5439792-3	Patent No. 5439792
57	50	56.2	20	6	5439792-8	Patent No. 5439792
58	49	55.1	9	3	US-08-108-709-23	Sequence 23, Appl
59	49	55.1	10	2	US-08-737-085A-10	Sequence 10, Appl
60	49	55.1	10	3	US-09-108-709-22	Sequence 22, Appl
61	49	55.1	10	4	US-09-246-258-10	Sequence 10, Appl
62	49	55.1	10	4	US-09-532-106-10	Sequence 10, Appl
63	49	55.1	10	4	US-09-839-666-10	Sequence 10, Appl
64	49	55.1	11	3	US-09-108-709-21	Sequence 21, Appl
65	49	55.1	12	2	US-08-146-028-176	Sequence 176, App
66	49	55.1	12	2	US-08-146-028-177	Sequence 177, App
67	49	55.1	12	4	US-08-723-425A-176	Sequence 176, App
68	49	55.1	12	4	US-08-723-425A-177	Sequence 177, App
69	49	55.1	12	4	US-09-112-206-176	Sequence 176, App
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71	48	53.9	13	4	US-08-682-791B-1	Sequence 1, Appl1
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73	47	52.8	12	1	US-07-633-964-3	Sequence 3, Appl1
74	47	52.8	12	1	US-08-386-956-3	Sequence 3, Appl1
75	47	52.8	12	3	US-09-108-709-34	Sequence 34, Appl
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77	47	52.8	13	3	US-09-108-709-36	Sequence 36, Appl
78	47	52.8	14	3	US-09-108-709-37	Sequence 37, Appl
79	46	51.7	11	3	US-09-108-709-37	Sequence 37, Appl
80	46	51.7	11	3	US-08-108-709-29	Sequence 29, Appl
81	45	50.6	12	2	US-08-682-791B-10	Sequence 10, Appl
82	45	50.6	12	2	US-08-146-028-24	Sequence 24, Appl
83	45	50.6	12	4	US-08-723-425A-24	Sequence 24, Appl
84	44	49.4	12	3	US-08-776-949-29	Sequence 29, Appl
85	43	48.3	11	3	US-08-776-949-38	Sequence 38, Appl
86	42	47.8	13	3	US-08-776-949-28	Sequence 28, Appl
87	42	47.2	15	1	US-07-633-964-9	Sequence 9, Appl1
88	42	47.2	15	1	US-08-386-956-9	Sequence 9, Appl1
89	42	47.2	15	3	US-09-108-709-13	Sequence 13, Appl
90	42	47.2	17	1	US-07-633-964-5	Sequence 5, Appl1
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92	42	47.2	17	2	US-08-833-546-1	Sequence 1, Appl1
93	42	47.2	17	3	US-09-108-709-6	Sequence 6, Appl1
94	42	47.2	17	3	US-08-386-956-1	Sequence 1, Appl1
95	42	47.2	19	2	US-08-765-452-8	Sequence 8, Appl1
96	41	46.1	10	1	US-07-633-964-21	Sequence 21, Appl
97	41	46.1	10	1	US-08-386-956-21	Sequence 21, Appl
98	41	46.1	10	3	US-09-108-709-16	Sequence 16, Appl
99	41	46.1	14	4	US-08-682-791B-6	Sequence 6, Appl1
100	41	46.1	14	4	US-08-682-791B-6	Sequence 6, Appl1

## ALIGNMENTS

## RESULT 1

US-08-615-279-8

Sequence 8, Application US/08615279

Patent No. 5804371

GENERAL INFORMATION:

APPLICANT: H SS, Eva

APPLICANT: SEIDEL, Christoph

APPLICANT: WIENHUES, Ursula-Henrike

APPLICANT: FAATZ, Elke

APPLICANT: SCHMITT, Urban

TITLE OF INVENTION: HAPTEN-LABELLED PEPTIDES

NUMBER OF SEQUENCES: 40

CORRESPONDENCE ADDRESSES:

ADDRESSEE: NIKAIIDO, MARCELSTEIN, MURRAY &amp; ORAM LLP

STREET: 655 Fifteenth Street, N. W., Suite 330 - G

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-5701

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/615,279

CLASSIFICATION: 435

FILING DATE: 25-MAR-1996

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: PCT/EP95/02921

FILING DATE: 24-JUL-1995

ATTORNEY/AGENT INFORMATION:

NAME: BERMAN, Richard J.

REGISTRATION NUMBER: 39,107

REFERENCE/DOCKET NUMBER: P564-6006

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202/638-5000

TELEFAX: 202/638-4810

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ORIGINAL SOURCE:

ORGANISM: Human immunodeficiency virus type 1

STRAIN: subtype O

POSITION IN GENOME:

CHROMOSOME/SEGMENT: 9p41

US-08-615-279-8

Query Match

Best Local Similarity 66.7%; Pred. NO. 7.9e-05;

Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 LNSWCKGRICVYTS 15

DB 1 LSLWCKGRKIVCYTS 15

RESULT 2

US-08-615-279-29

Sequence 29, Application US/08615279

Patent No. 5804371

GENERAL INFORMATION:

APPLICANT: H SS, Eva

APPLICANT: SEIDEL, Christoph

APPLICANT: WIENHUES, Ursula-Henrike

APPLICANT: FAATZ, Elke

APPLICANT: SCHMITT, Urban

TITLE OF INVENTION: HAPTEN-LABELLED PEPTIDES

NUMBER OF SEQUENCES: 40

CORRESPONDENCE ADDRESSES:

ADDRESSEE: NIKAIIDO, MARCELSTEIN, MURRAY &amp; ORAM LLP

STREET: 655 Fifteenth Street, N. W., Suite 330 - G

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-5701

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/615,279

FILING DATE: 25-MAR-1996

CLASSIFICATION: 435

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: PCT/EP95/02921

FILING DATE: 24-JUL-1995

ATTORNEY/AGENT INFORMATION:

NAME: BERMAN, Richard J.

REGISTRATION NUMBER: 39,107

REFERENCE/DOCKET NUMBER: P564-6006

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202/638-5000

TELEFAX: 202/638-4810

INFORMATION FOR SEQ ID NO: 29:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

FEATURE:

NAME/KEY: Modified-site

LOCATION: 1

OTHER INFORMATION: /note=

OTHER INFORMATION: "digoxigenin-3-cme-beta-alanine-epsilon-aminocaproic

OTHER INFORMATION: acid-beta-alanine is attached to the Leu at the 1 position

US-08-615-279-29

Query Match

Best Local Similarity 66.7%; Pred. NO. 7.9e-05;

Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 LNSWCKGRICVYTS 15

DB 1 LSLWCKGRKIVCYTS 15

RESULT 3

US-08-472-597A-4

Sequence 4, Application US/08472597A

Patent No. 5624797

GENERAL INFORMATION:

APPLICANT: Bridon, D.P.

APPLICANT: Size, I.S.Y.

APPLICANT: Dagfal, D.J.

APPLICANT: Jaffe, K.D.

APPLICANT: Colpitts, T.L.

TITLE OF INVENTION: Peptides for HIV-1 Detection

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESSES:

ADDRESSEE: ABBOTT LABORATORIES

STREET: ONE HUNDRED ABBOTT PARK ROAD

CITY: ABBOTT PARK

STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/472.597A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: FOREMSKI, PRISCILLA E.  
REGISTRATION NUMBER: 33,207  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 708-937-6365  
TELEFAX: 708-938-2623  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-472-597A-4

Query Match 76.4%; Score 68; DB 1; Length 19;  
Best Local Similarity 71.4%; Pred. No. 0.00039;  
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LNSWCGKGRILCYT 14  
| |||||:||||  
Db 6 LGIWGCKGKILCYT 19

## RESULT 4

US-08-837-732-4  
Sequence 4, Application US/08837732  
Patent No. 5800983  
GENERAL INFORMATION:  
APPLICANT: Bridon, D.P.  
APPLICANT: Size, I.S.Y.  
APPLICANT: Dagbafal, D.J.  
APPLICANT: Jaffe, K.D.  
APPLICANT: Colpitts, T.L.  
TITLE OF INVENTION: Peptides for HIV-1 Detection  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ABBOTT LABORATORIES  
STREET: ONE HUNDRED ABBOTT PARK ROAD  
CITY: ABBOTT PARK  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/837.732  
FILING DATE: 22-APR-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/472.597  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: FOREMSKI, PRISCILLA E.  
REGISTRATION NUMBER: 33,207  
REFERENCE/DOCKET NUMBER: 5765.US.01  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 708-937-6365  
TELEFAX: 708-938-2623  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-837-732-4

Query Match 76.4%; Score 68; DB 1; Length 19;  
Best Local Similarity 71.4%; Pred. No. 0.00039;  
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LNSWCGKGRILCYT 14  
| |||||:||||  
Db 6 LGIWGCKGKILCYT 19

## RESULT 5

US-08-472-597A-3  
Sequence 3, Application US/08472597A  
Patent No. 5624797  
GENERAL INFORMATION:  
APPLICANT: Bridon, D.P.  
APPLICANT: Size, I.S.Y.  
APPLICANT: Dagbafal, D.J.  
APPLICANT: Jaffe, K.D.  
APPLICANT: Colpitts, T.L.  
TITLE OF INVENTION: Peptides for HIV-1 Detection  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ABBOTT LABORATORIES  
STREET: ONE HUNDRED ABBOTT PARK ROAD  
CITY: ABBOTT PARK  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/472.597A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: FOREMSKI, PRISCILLA E.  
REGISTRATION NUMBER: 33,207  
REFERENCE/DOCKET NUMBER: 5765.US.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 708-937-6365  
TELEFAX: 708-938-2623  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-472-597A-3

Query Match 70.8%; Score 63; DB 1; Length 19;  
Best Local Similarity 64.3%; Pred. No. 0.0022;  
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 LNSWCGKGRILCYT 14  
| |||||:||||  
Db 6 LGIWGCKGKILCYT 19

STATE: IL

TELEPHONE: 706-937-0502

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? TELEFAX: 708-938-2623
? INFORMATION FOR SEQ ID NO: 2:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 19 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: protein
US-08-837-732-2

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Query Match	66.3%	Score 59;	DB 1;	Length 19;
Best Local Similarity	64.3%	Pred. No. 0.0088;		
Matches	9;	Conservative	2;	Mismatches 3;
				Indels 0;
				Gaps 0

QY	1	LNSWGCKGRITCYT	14
		: :	
Db	6	LGIWGCKGKLICTT	19

RESULT 9  
US-08-682

Sequence 7, Application US/08682791B  
Patent No. 6210901  
GENERAL INFORMATION:  
APPLICANT: SEIDEL, Christoph;  
APPLICANT: HERMANN, Rupert;  
APPLICANT: HOESS, Eva;  
APPLICANT: BARTZ, Hans-Georg;  
TITLE OF INVENTION: SPECIFIC BINDING SUBSTANCES FOR ANTIBODIES;  
TITLE OF INVENTION: AND THEIR USE FOR IMMUNOASSAYS OR VACCINES;  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:

OTHER INFORMATION: Xaa is p-fluor-phenylalanine  
US-08-682-791B-7

```

OY      2 NSWGCKGRICYTS 15
         ||||| | :|:|:
Db      1 NSWGCAXRQVCHTT 14

```

RESULT 10  
US-08-682-791B-8

Patent No. 6210901  
 GENERAL INFORMATION:  
 APPLICANT: SEIDEL, Christoph;  
 APPLICANT: HERRMANN, Rupert;  
 APPLICANT: HOESS, Eva;  
 APPLICANT: BATZ Han-Georg;  
 TITLE OF INVENTION: SPECIFIC BINDING SUBSTANCES FOR ANTIBODIES  
 TITLE OF INVENTION: AND THEIR USE FOR IMMUNOASSAYS OR VACCINES  
 NUMBER OF SEQUENCES: 33  
 CORRESPONDENCE ADDRESS:

Query Match	62.98;	Score 56;	DB 4;	Length 14;
Best Local Similarity	57.18;	Pred. No. 0.019;		
Matches	8;	Conservative	3;	Mismatches 3. Indels 0. Cons 0

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      2 NSWGCKGRICYTS 15
      ||||| | :|:|:
      1 NSWGCAXRQVCHTT 14

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RESULT 11  
S-08-682-791B-11

Sequence 11, Application US/08682791B  
Patent No. 6210901

GENERAL INFORMATION:

APPLICANT: SEIDEL, Christoph;  
APPLICANT: HERMANN, Rupert;  
APPLICANT: HOESS, Eva;  
APPLICANT: BATZ, Han-Georg  
TITLE OF INVENTION: SPECIFIC BINDING SUBSTANCES FOR ANTIBODIES  
TITLE OF INVENTION: AND THEIR USE FOR IMMUNASSAYS OR VACCINES  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:

CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10022

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/682,791B  
FILING DATE: July 31, 1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 6210901man D. Hanson  
REGISTRATION NUMBER: 30,946  
REFERENCE/DOCKET NUMBER: HUBR 1092  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 688-9200  
TELEFAX: (212) 638-3884  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14  
TYPE: amino acids  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
OTHER INFORMATION: Xaa is Nle  
US-08-682-791B-11

Query Match 61.8%; Score 55; DB 4; Length 14;  
Best Local Similarity 57.1%; Pred. No. 0.026;  
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 2 NSWGCKGRILCYTS 15  
DB 1 NSWGCAFRXLCHTT 14

RESULT 12  
US-08-615-279-27  
Sequence 27, Application US/08615279  
Patent No. 5804371  
GENERAL INFORMATION:  
APPLICANT: H SS, Eva  
APPLICANT: SEIDEL, Christoph  
APPLICANT: WIENHUES, Ursula-Henrike  
APPLICANT: PAATZ, Elke  
APPLICANT: SCHMITT, Urban  
TITLE OF INVENTION: HAPTEN-LABELLED PEPTIDES  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIKAIIDO, MARMELESTEIN, MURRAY & ORAM LLP  
STREET: 655 Fifteenth Street, N. W., Suite 330 - G  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-5701  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/615,279  
FILING DATE: 25-MAR-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP95/02921  
FILING DATE: 24-JUL-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: BERMAN, Richard J.  
REGISTRATION NUMBER: 39,107  
REFERENCE/DOCKET NUMBER: P564-6006  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202/638-5000

TELEFAX: 202/638-4810  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1  
OTHER INFORMATION: /note-  
OTHER INFORMATION: "digoxigenin-3-cme-beta-alanine-epsilon-aminocaproic  
OTHER INFORMATION: acid-beta-alanine is attached to the Leu at the 1 position  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 10  
OTHER INFORMATION: /note-  
OTHER INFORMATION: "cme-3-digoxigenin 1s  
OTHER INFORMATION: attached to the Leu at the 10 position."  
US-08-615-279-27

Query Match 61.8%; Score 55; DB 1; Length 16;  
Best Local Similarity 53.3%; Pred. No. 0.03;  
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 LNSWGCKGRILCYTS 15  
DB 1 LGIWGCKGSKLICTTA 15

RESULT 13  
US-08-765-452-7  
Sequence 7, Application US/08765452  
Patent No. 5981286  
GENERAL INFORMATION:  
APPLICANT: HERRMANN, Rupert  
APPLICANT: JOSEL, Hans-Peter  
APPLICANT: FAUPER, Gunter  
APPLICANT: VOGTLE, Fritz  
APPLICANT: FROMMERBERGER, Bruno  
APPLICANT: ISSBERNER, Jorg  
TITLE OF INVENTION: HYDROPHILIC METAL COMPLEXES  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIKAIIDO, MARMELESTEIN, MURRAY & ORAM LLP  
STREET: 655 15th Street, N.W., Suite 330 - G.St.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-5701  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/765,452  
FILING DATE: 16-JAN-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: JAHNS, Kristina M.  
REGISTRATION NUMBER: 41,092  
REFERENCE/DOCKET NUMBER: 564-6014  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 638-5000  
TELEFAX: (202) 638-4810  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear



MOLECULE TYPE: peptide  
US-08-765-452-7

Query Match 61.8%; Score 55; DB 2; Length 16;  
Best Local Similarity 53.3%; Pred. No. 0.03;  
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 NSMCGKRIICYS 15  
DB 1 LGIMCGSKLICHTA 15

## RESULT 14

US-08-615-279-32

Sequence 32, Application US/08615279  
Patent No. 5804371  
GENERAL INFORMATION:  
APPLICANT: H SS, Eva  
APPLICANT: SEIDEL, Christoph  
APPLICANT: WIENHUES, Ursula-Henrike  
APPLICANT: RAATZ, Elke  
APPLICANT: SCHMITT, Urban  
TITLE OF INVENTION: HAPTEN-LABELLED PEPTIDES  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIKAIKO, MARIELSTEIN, MURRAY & ORAM LLP  
STREET: 655 Fifteenth Street, N. W., Suite 330 - G  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-5701  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/615,279  
FILING DATE: 25-MAR-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP95/02921  
FILING DATE: 24-JUL-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: BERMAN, Richard J.  
REGISTRATION NUMBER: 39,107  
REFERENCE/DOCKET NUMBER: P564-6006  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202/638-5000  
TELEFAX: 202/638-4810  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1  
OTHER INFORMATION: /note=  
OTHER INFORMATION: "digoxigenin-3-cme-epsilon-amino caproic acid is attached to  
OTHER INFORMATION: asn at the 1 position."  
US-08-615-279-32

Query Match 60.7%; Score 54; DB 1; Length 14;  
Best Local Similarity 57.1%; Pred. No. 0.037;  
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 2 NSMCGKRIICYS 15  
DB 1 NSMCGAFROVCHTT 14

## RESULT 15

US-08-765-452-11

Sequence 11, Application US/08765452  
Patent No. 5981286  
GENERAL INFORMATION:  
APPLICANT: HERRMANN, Rupert  
APPLICANT: JOSEL, Hans-Peter  
APPLICANT: PAPPERT, Gunter  
APPLICANT: VOSTER, Fritz  
APPLICANT: FROMBERGER, Bruno  
APPLICANT: ISSBERNER, Jorg  
TITLE OF INVENTION: HYDROPHILIC METAL COMPLEXES  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIKAIKO, MARIELSTEIN, MURRAY & ORAM LLP  
STREET: 655 15th Street, N.W., Suite 330 - G St.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-5701  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/765,452  
FILING DATE: 16-JAN-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: JAHNS, Kristina M.  
REGISTRATION NUMBER: 41,092  
REFERENCE/DOCKET NUMBER: 564-6014  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 638-5000  
TELEFAX: (202) 638-4810  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-765-452-11

Query Match 60.7%; Score 54; DB 2; Length 14;  
Best Local Similarity 57.1%; Pred. No. 0.037;  
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 2 NSMCGKRIICYS 15  
DB 1 NSMCGAFROVCHTT 14

## RESULT 16

US-07-633-964-8

Sequence 8, Application US/07633964  
Patent No. 5459060  
GENERAL INFORMATION:  
APPLICANT: COLTOPA MD, Joseph P  
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES DIRECTED  
TITLE OF INVENTION: IMMUNODEFICIENCY VIRUS (HIV-1)  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Charles S. Coltopa, Esq.  
STREET: 1201 Elm Street, Suite 4500  
CITY: Dallas  
STATE: TX  
COUNTRY: USA

ZIP: 75270-2197  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/633,964  
FILING DATE: 19901226  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 396751  
FILING DATE: 24-AUG-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Cotriopia, Charles S  
REGISTRATION NUMBER: 27189  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (214) 939-4500  
TELEFAX: (214) 939-4600  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
FRAGMENT TYPE: Internal  
US-07-633-964-8

Query Match 60.7%; Score 54; DB 1; Length 15;  
Best Local Similarity 57.1%; Pred. No. 0.039;  
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 LNSWCKGRITCYT 14  
| | | | | | | | | | | | | | | | |  
DB 2 LGIWGCSGKLICTT 15

RESULT 17  
US-08-386-956-8  
Sequence 8, Application US/08386956  
Patent No. 5777074  
GENERAL INFORMATION:  
APPLICANT: Cotriopia MD, Joseph P  
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES DIRECTED  
AGAINST THE TRANSMEMBRANE GLYCOPROTEIN (gp41) OF HUMAN  
IMMUNODEFICIENCY VIRUS (HIV-1)  
TITLE OF INVENTION: AGAINST THE TRANSMEMBRANE GLYCOPROTEIN (gp41) OF HUMAN  
IMMUNODEFICIENCY VIRUS (HIV-1)  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Charles S. Cotriopia, Esq.  
STREET: 1201 Elm Street, Suite 4500  
CITY: Dallas  
STATE: TX  
COUNTRY: USA  
ZIP: 75270-2197  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/386,956  
FILING DATE: 10-FEB-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/633964  
FILING DATE: 26-DEC-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Cotriopia, Charles S  
REGISTRATION NUMBER: 27189  
REFERENCE/DOCKET NUMBER: CLON B-28796CIPC  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (214) 939-4500  
TELEFAX: (214) 939-4600  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
FRAGMENT TYPE: Internal  
US-08-386-956-8

Query Match 60.7%; Score 54; DB 1; Length 15;  
Best Local Similarity 57.1%; Pred. No. 0.039;  
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 LNSWCKGRITCYT 14  
| | | | | | | | | | | | | | | | |  
DB 2 LGIWGCSGKLICTT 15

RESULT 18  
US-09-108-709-12  
Sequence 12, Application US/09108709  
Patent No. 6008044  
GENERAL INFORMATION:  
APPLICANT: Cotriopia, Joseph P.  
TITLE OF INVENTION: Human Monoclonal Antibodies Directed Against the Transmembrane  
GLYCOPROTEIN (gp41) of Human Immunodeficiency Virus-1 (HIV-1) and Prognosis  
TITLE OF INVENTION: Detecting the Presence and Concentration of Antibodies Inhibit  
FILE REFERENCE: 10586/00406  
CURRENT APPLICATION NUMBER: US/09/108,709  
CURRENT FILING DATE: 1998-07-01  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 12  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Human immunodeficiency virus type 1  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (1)-(15)  
OTHER INFORMATION: amino acids 597-611 according to the Gnaun  
OTHER INFORMATION: numbering system  
US-09-108-709-12

Query Match 60.7%; Score 54; DB 3; Length 15;  
Best Local Similarity 57.1%; Pred. No. 0.039;  
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 LNSWCKGRITCYT 14  
| | | | | | | | | | | | | | | | |  
DB 2 LGIWGCSGKLICTT 15

RESULT 19  
US-08-472-597A-1  
Sequence 1, Application US/08472597A  
Patent No. 5624797  
GENERAL INFORMATION:  
APPLICANT: Bridon, D.P.  
APPLICANT: Size, I.S.Y.  
APPLICANT: Daghfal, D.J.  
APPLICANT: Jaffe, K.D.  
APPLICANT: Colpitts, T.L.  
TITLE OF INVENTION: Peptides for HIV-1 Detection  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ABBOTT LABORATORIES  
STREET: ONE HUNDRED ABBOTT PARK ROAD  
CITY: ABBOTT PARK  
STATE: IL

COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/472.597A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: FOREMSKI, PRISCILLA E.  
REGISTRATION NUMBER: 33,207  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 708-937-6365  
TELEFAX: 708-938-2623  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-472-597A-1

Query Match 60.7%; Score 54; DB 1; Length 19;  
Best Local Similarity 57.1%; Pred. No. 0.049;  
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 LNSWGCKGRITCT 14  
DB 6 LGTWGCKGLICTT 19

RESULT 20  
US-08-837-732-1  
Sequence 1, Application US/08837732  
Patent No. 5800983  
GENERAL INFORMATION:  
APPLICANT: Bridon, D.P.  
APPLICANT: Size, I.S.Y.  
APPLICANT: Daghefal, D.J.  
APPLICANT: Jaffe, K.D.  
APPLICANT: Colpitts, T.L.  
TITLE OF INVENTION: Peptides for HIV-1 Detection  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ABBOTT LABORATORIES  
STREET: ONE HUNDRED ABBOTT PARK ROAD  
CITY: ABBOTT PARK  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/837.732  
FILING DATE: 22-APR-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/472.597  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: FOREMSKI, PRISCILLA E.  
REGISTRATION NUMBER: 33,207  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 708-937-6365

TELEFAX: 708-938-2623  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-837-732-1

Query Match 60.7%; Score 54; DB 1; Length 19;  
Best Local Similarity 57.1%; Pred. No. 0.049;  
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 LNSWGCKGRITCT 14  
DB 6 LGTWGCKGLICTT 19

RESULT 21  
US-08-146-028-5  
Sequence 5, Application US/08146028  
Patent No. 5891640  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES  
CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THE  
TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED  
TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES  
NUMBER OF SEQUENCES: 453  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/146.028  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: Ant170  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 12  
US-08-146-028-5

Query Match 59.6%; Score 53; DB 2; Length 12;  
Best Local Similarity 66.7%; Pred. No. 0.045;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 WCKGKRIIC 12  
DB 3 WCKGKRLVC 11

RESULT 22  
US-08-723-425A-5  
Sequence 5, Application US/08723425A  
Patent No. 6165730  
GENERAL INFORMATION:  
APPLICANT: DELEYS, ROBERT  
TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF  
TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT  
TITLE OF INVENTION: EPITOPES AND THEIR USE IN A PROCESS FOR DETERMINATION OF

TITLE OF INVENTION: ANTIBODIES OR BIOTINYLATED PEPTIDES CORRESPONDING ...  
NUMBER OF SEQUENCES: 433  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: NIXON & VANDERHAYE, P.C.  
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
CITY: Arlington  
STATE: VA  
COUNTRY: USA  
ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/723,425A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: SAOOF, B.J.  
REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 1487-13  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-816-4000  
TELEFAX: 703-816-4100  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: Ant70  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1  
NAME/KEY: Modified-site  
LOCATION: 12  
US-08-723-425A-5

Query Match 59.6%; Score 53; DB 4; Length 12;  
Best Local Similarity 66.7%; Pred. No. 0.045;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 WCGKGRITC 12  
|||||:::|  
DB 3 WCGKGRITC 11

RESULT 23  
US-09-112-206-5  
Sequence 5, Application US/09112206  
Patent No. 6210903  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES  
CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR  
TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED  
PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,  
TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM  
NUMBER OF SEQUENCES: 453  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/112,206  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/146,028

FILING DATE:  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: Ant70  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1  
NAME/KEY: Modified-site  
LOCATION: 12  
US-09-112-206-5

Query Match 59.6%; Score 53; DB 4; Length 12;  
Best Local Similarity 66.7%; Pred. No. 0.045;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 WCGKGRITC 12  
|||||:::|  
DB 3 WCGKGRITC 11

RESULT 24  
US-09-009-953-131  
Sequence 131, Application US/09009953  
Patent No. 6413517  
GENERAL INFORMATION:  
APPLICANT: Sette, Alessandro  
TITLE OF INVENTION: Identification of Broadly  
Reactive DR Restricted Epitopes  
NUMBER OF SEQUENCES: 274  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/009,953  
FILING DATE: 21-Jan-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/036,713  
FILING DATE: 23-JAN-1997  
APPLICATION NUMBER: US 60/037,432  
FILING DATE: 07-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Ellen Lauver  
REGISTRATION NUMBER: 32,762  
REFERENCE/DOCKET NUMBER: 018623-011520US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-576-0200  
TELEFAX: 415-576-0300  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 131:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 131:

US-09-009-953-131

Query Match 59.6%; Score 53; DB 4; Length 16;  
Best Local Similarity 58.3%; Pred. No. 0.059;  
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 4 WCGKGRICYS 15  
||| |::||| |:  
DB 1 WCGSGKLICTTA 12

RESULT 25

US-07-901-874B-14  
; Sequence 14, Application US/07901874B  
; Patent No. 5476765

GENERAL INFORMATION:  
APPLICANT: Chang Y1 Wang  
TITLE OF INVENTION: SYNTHETIC PEPTIDE COMPOSITIONS  
TITLE OF INVENTION: WITH IMMUNOREACTIVITIES TO ANTIBODIES TO HTLV AND AS  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154

COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/901,874B  
FILING DATE: 22-JUN-1992

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/469,291  
FILING DATE: 24-JAN-1990

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/297,635  
FILING DATE: 13-JAN-1989

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/001,885  
FILING DATE: 9-JAN-1987

CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MARIA C. H. LIN

REGISTRATION NUMBER: 29,323  
REFERENCE/DOCKET NUMBER: 1151-4026 US1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849

INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19  
TYPE: Amino acid  
STRANDEDNESS: Single  
TOPOLOGY: Unknown

MOLECULE TYPE: Peptide  
US-07-901-874B-14

Query Match 59.6%; Score 53; DB 1; Length 19;  
Best Local Similarity 58.3%; Pred. No. 0.07;  
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 4 WCGKGRICYS 15  
||| |::||| |:  
DB 2 WCGSGKLICTTA 13

RESULT 26

US-08-457-865-14  
; Sequence 14, Application US/08457865  
; Patent No. 5681696

GENERAL INFORMATION:  
APPLICANT: Chang Y1 Wang  
TITLE OF INVENTION: SYNTHETIC PEPTIDE COMPOSITIONS  
TITLE OF INVENTION: WITH IMMUNOREACTIVITIES TO ANTIBODIES TO HTLV AND AS  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154

COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/457,865  
FILING DATE:

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,874  
FILING DATE: 22-JUN-1992

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/469,291  
FILING DATE: 24-JAN-1990

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/297,635  
FILING DATE: 13-JAN-1989

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/001,885  
FILING DATE: 9-JAN-1987

CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MARIA C. H. LIN  
REGISTRATION NUMBER: 29,323  
REFERENCE/DOCKET NUMBER: 1151-4026 US1

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19  
TYPE: Amino acid  
STRANDEDNESS: Single  
TOPOLOGY: Unknown

MOLECULE TYPE: Peptide  
US-08-457-865-14

Query Match 59.6%; Score 53; DB 1; Length 19;  
Best Local Similarity 58.3%; Pred. No. 0.07;  
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 4 WCGKGRICYS 15  
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DB 2 WCGSGKLICTTA 13

RESULT 27

US-07-633-964-14  
; Sequence 14, Application US/07633964  
; Patent No. 5458060

GENERAL INFORMATION:  
APPLICANT: Coltopia MD, Joseph P  
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES DIRECTED  
TITLE OF INVENTION: IMMUNODEFICIENCY VIRUS (HIV-1)  
NUMBER OF SEQUENCES: 42

;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Charles S. Cotropia, Esq.  
;; STREET: 1201 Elm Street, Suite 4500  
;; CITY: Dallas  
;; STATE: TX  
;; COUNTRY: USA  
;; ZIP: 75270-2197  
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;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
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;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/07/633,964  
;; FILING DATE: 19901226  
;; CLASSIFICATION: 424  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 396751  
;; FILING DATE: 24-AUG-1989  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Cotropia, Charles S  
;; REGISTRATION NUMBER: 27189  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (214) 939-4500  
;; TELEFAX: (214) 939-4600  
;; INFORMATION FOR SEQ ID NO: 14:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 20 amino acids  
;; TYPE: AMINO ACID  
;; TOPOLOGY: circular  
;; MOLECULE TYPE: peptide  
;; HYPOTHEICAL: NO  
;; FRAGMENT TYPE: Internal  
;; US-07-633-964-14  
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;; Query Match 59.6%; Score 53; DB 1; Length 20;  
;; Best Local Similarity 58.3%; Pred. No. 0.073;  
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
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DB 3 WCGSGKLICTTA 14  
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RESULT 28  
US-08-386-956-14  
; Sequence 14, Application US/08386956  
; Patent No. 5777074  
; GENERAL INFORMATION:  
; APPLICANT: Cotropia MD, Joseph P  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES DIRECTED  
; TITLE OF INVENTION: AGAINST THE TRANSMEMBRANE GLYCOPROTEIN (gp41) OF HUMAN  
; TITLE OF INVENTION: IMMUNODEFICIENCY VIRUS (HIV-1)  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Charles S. Cotropia, Esq.  
; STREET: 1201 Elm Street, Suite 4500  
; CITY: Dallas  
; STATE: TX  
; COUNTRY: USA  
; ZIP: 75270-2197  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/386,956  
; FILING DATE: 10-FEB-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/633964

;; FILING DATE: 26-DEC-1990  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Cotropia, Charles S  
;; REGISTRATION NUMBER: 27189  
;; REFERENCE/DOCKET NUMBER: CLON B-28796CIPC  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (214) 939-4500  
;; TELEFAX: (214) 939-4600  
;; INFORMATION FOR SEQ ID NO: 14:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 20 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: circular  
;; MOLECULE TYPE: peptide  
;; HYPOTHEICAL: NO  
;; FRAGMENT TYPE: Internal  
;; US-08-386-956-14  
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;; Query Match 59.6%; Score 53; DB 1; Length 20;  
;; Best Local Similarity 58.3%; Pred. No. 0.073;  
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
QY 4 WCGGRIICYS 15  
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DB 3 WCGSGKLICTTA 14  
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RESULT 29  
US-09-108-709-45  
; Sequence 45, Application US/09108709  
; Patent No. 6008044  
; GENERAL INFORMATION:  
; APPLICANT: Cotropia, Joseph P.  
; TITLE OF INVENTION: Human Monoclonal Antibodies Directed Against the Transmembrane  
; TITLE OF INVENTION: (gp41) of Human Immunodeficiency Virus-1 (HIV-1) and Prognosis  
; TITLE OF INVENTION: Detecting the Presence and Concentration of Antibodies Inhibit  
; FILE REFERENCE: 10586/00406  
; CURRENT FILING DATE: 1998-07-01  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 45  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus type 1  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (1)..(20)  
; OTHER INFORMATION: amino acids 599-618 according to Gann numbering  
; OTHER INFORMATION: system  
; US-09-108-709-45  
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;; Query Match 59.6%; Score 53; DB 3; Length 20;  
;; Best Local Similarity 58.3%; Pred. No. 0.073;  
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
QY 4 WCGGRIICYS 15  
||| |::||| |:  
DB 3 WCGSGKLICTTA 14  
;;  
RESULT 30  
US-08-146-028-2  
; Sequence 2, Application US/08146028  
; Patent No. 5891640  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES  
; TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THE  
; TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYATE  
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPE  
; TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM

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NUMBER OF SEQUENCES: 453
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/146,028
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: HIV-1
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
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NAME/KEY: Modified-site
LOCATION: 21
US-08-146-028-2

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Query Match      59.68; Score 53; DB 2; Length 21;
Best Local Similarity 58.38; Pred. No. 0.076;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
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Db      3 WCGSGKLCITTA 14

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Job time : 15 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 5, 2003, 07:21:57 ; Search time 228 Seconds  
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6.792 Million cell updates/sec

Title: US-09-605-573a-69\_COPY\_12\_26  
Perfect score: 89  
Sequence: 1 LNSWCKGRITCYTS 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 392085 seqs, 103240269 residues

Total number of hits satisfying chosen parameters: 80475

Minimum DB seq length: 0  
Maximum DB seq length: 21

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 100 summaries

## Database :

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3: /cgn2\_6/ptodata/1/pubppaa/US06\_NEW\_PUB pep:\*  
4: /cgn2\_6/ptodata/1/pubppaa/US06\_PUBCOMB pep:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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2	53	59.6	16	9	US-09-423-863-5
3	52	58.4	16	9	US-09-423-863-4
4	51	57.3	21	9	US-09-845-042-23
5	50	56.2	16	9	US-09-423-863-3
6	50	56.2	16	9	US-09-423-863-6
7	49	55.1	10	10	US-09-839-666-10
8	49	55.1	16	9	US-09-423-863-1
9	42	47.2	17	9	US-09-388-847-1
10	40	44.9	9	1	US-08-821-739A-78
11	40	44.9	9	10	US-09-894-018-80
12	40	44.9	9	10	US-09-894-018-185
13	37	41.6	10	10	US-09-765-086-43
14	36	40.4	6	9	US-10-026-741-41
15	35	39.3	10	1	US-08-821-739A-90
16	35	39.3	20	9	US-09-910-009A-481
17	34	38.2	7	9	US-10-026-741-5
18	34	38.2	10	9	US-09-423-863-10
19	34	38.2	10	9	US-09-423-863-11

20	33	37.1	10	9	US-09-423-863-9	Sequence 9, Appl
21	33	37.1	10	9	US-09-845-612B-14	Sequence 14, Appl
22	31	34.8	15	9	US-09-423-863-8	Sequence 8, Appl
23	31	34.8	13	9	US-09-910-009A-416	Sequence 416, Appl
24	31	34.8	18	9	US-10-142-238A-49	Sequence 49, Appl
25	30	33.7	10	9	US-09-423-863-7	Sequence 7, Appl
26	30	33.7	10	9	US-09-572-004B-922	Sequence 922, Appl
27	30	33.7	14	10	US-09-969-192-68	Sequence 68, Appl
28	30	33.7	21	9	US-09-974-879-281	Sequence 281, Appl
29	30	33.7	21	9	US-09-305-736-269	Sequence 269, Appl
30	29	32.6	14	9	US-09-999-724-93	Sequence 93, Appl
31	29	32.6	15	10	US-09-073-009-59	Sequence 59, Appl
32	29	32.6	15	10	US-09-023-588-58	Sequence 58, Appl
33	29	32.6	15	10	US-09-793-306-59	Sequence 59, Appl
34	29	32.6	15	10	US-09-969-192-68	Sequence 58, Appl
35	29	32.6	16	10	US-09-023-588-58	Sequence 58, Appl
36	29	32.6	16	10	US-09-793-306-58	Sequence 58, Appl
37	28.5	32.0	18	9	US-09-801-485-9	Sequence 9, Appl
38	28	31.5	10	9	US-10-046-922-35	Sequence 35, Appl
39	28	31.5	13	10	US-09-911-838-214	Sequence 214, Appl
40	28	31.5	15	9	US-10-098-093-110	Sequence 110, Appl
41	28	31.5	16	9	US-09-910-009A-247	Sequence 247, Appl
42	28	31.5	21	9	US-09-974-879-326	Sequence 326, Appl
43	28	31.5	21	10	US-09-305-736-326	Sequence 326, Appl
44	28	31.5	21	10	US-09-864-761-36483	Sequence 36483, A
45	27.5	30.9	10	9	US-09-813-653-40	Sequence 40, Appl
46	27	30.3	9	10	US-09-840-277-22	Sequence 22, Appl
47	27	30.3	10	10	US-09-354-597A-18	Sequence 18, Appl
48	27	30.3	10	12	US-10-003-405-5	Sequence 5, Appl
49	27	30.3	12	10	US-09-784-887B-5	Sequence 5, Appl
50	27	30.3	13	9	US-10-087-714-4	Sequence 4, Appl
51	27	30.3	13	9	US-10-185-050-69	Sequence 69, Appl
52	27	30.3	14	9	US-10-029-301-5	Sequence 31, Appl
53	27	30.3	14	9	US-09-929-266-73	Sequence 73, Appl
54	27	30.3	15	9	US-09-932-613-74	Sequence 74, Appl
55	27	30.3	17	9	US-09-910-009A-426	Sequence 426, Appl
56	27	30.3	17	10	US-09-864-761-41378	Sequence 41378, A
57	27	30.3	18	9	US-09-910-009A-427	Sequence 427, Appl
58	27	30.3	19	9	US-10-092-750-245	Sequence 245, Appl
59	27	30.3	19	10	US-09-864-761-48238	Sequence 48238, A
60	27	30.3	20	8	US-09-864-761-44019	Sequence 44019, A
61	26	29.2	5	9	US-08-239-765B-4	Sequence 4, Appl
62	26	29.2	5	9	US-09-042-888B-2	Sequence 2, Appl
63	26	29.2	5	9	US-09-949-278-2	Sequence 2, Appl
64	26	29.2	5	10	US-10-300-757-23	Sequence 23, Appl
65	26	29.2	8	9	US-09-815-156-2	Sequence 2, Appl
66	26	29.2	8	9	US-10-094-401-182	Sequence 182, Appl
67	26	29.2	9	10	US-09-835-948-38	Sequence 38, Appl
68	26	29.2	9	10	US-09-920-174-42	Sequence 42, Appl
69	26	29.2	10	9	US-09-572-404B-2155	Sequence 2155, Ap
70	26	29.2	11	10	US-09-780-070-26	Sequence 26, Appl
71	26	29.2	11	10	US-10-059-261-297	Sequence 297, App
72	26	29.2	12	9	US-10-094-401-230	Sequence 230, App
73	26	29.2	14	10	US-09-747-029A-18	Sequence 18, Appl
74	26	29.2	15	9	US-10-090-049-14	Sequence 14, Appl
75	26	29.2	15	9	US-09-997-961-18	Sequence 18, Appl
76	26	29.2	15	9	US-09-997-961-20	Sequence 20, Appl
77	26	29.2	15	9	US-09-997-961-25	Sequence 25, Appl
78	26	29.2	15	12	US-09-997-961-27	Sequence 27, Appl
79	26	29.2	15	12	US-10-028-051-14	Sequence 14, Appl
80	26	29.2	16	9	US-09-910-009A-408	Sequence 408, App
81	26	29.2	17	9	US-09-846-091-8	Sequence 8, Appl
82	26	29.2	17	9	US-10-012-756-16	Sequence 16, Appl
83	26	29.2	18	10	US-09-864-761-38674	Sequence 38674, A
84	26	29.2	18	10	US-09-747-029A-17	Sequence 17, Appl
85	26	29.2	19	10	US-09-864-761-37007	Sequence 37007, A
86	26	29.2	20	8	US-08-592-711-8	Sequence 8, Appl
87	26	29.2	20	8	US-09-843-676-194	Sequence 194, App
88	26	29.2	20	9	US-09-973-025-75	Sequence 75, Appl

93	26	29.2	20	9	US-09-438-486-194	Sequence 194, App
94	26	29.2	20	9	US-10-053-758-194	Sequence 194, App
95	26	29.2	20	9	US-09-899-303-75	Sequence 75, Appl
96	26	28.2	20	9	US-10-054-295-194	Sequence 194, App
97	26	28.2	20	9	US-10-083-357-1028	Sequence 1028, App
98	26	29.2	20	9	US-10-054-611-194	Sequence 194, App
99	26	29.2	20	9	US-10-023-282-902	Sequence 902, App
100	26	29.2	20	9	US-09-955-808-75	Sequence 75, Appl

## ALIGNMENTS

RESULT 1  
US-09-423-863-2  
Sequence 2, Application US/09423863  
Publication No. US20030054336A1  
GENERAL INFORMATION:  
APPLICANT: Donie, Frederic  
APPLICANT: Faatz, Elke  
APPLICANT: Hoess, Eva  
TITLE OF INVENTION: PROCESS FOR THE DETECTION OF HIV ANTIBODIES AND  
FILE REFERENCE: BMID 9974 4638/OP/US-Sz  
CURRENT APPLICATION NUMBER: US/09/423,863  
CURRENT FILING DATE: 2000-02-08  
EARLIER APPLICATION NUMBER: DE 19720914.9  
EARLIER FILING DATE: 1997-05-16  
EARLIER APPLICATION NUMBER: PCT/EP98/02816  
EARLIER FILING DATE: 1998-05-13  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Human immunodeficiency virus type 1  
US-09-423-863-2

Query Match 59.6%; Score 53; DB 9; Length 16;  
Best Local Similarity 60.0%; Pred. No. 0.078;  
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

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DB 1 LGIWGSGRHICTT 15

RESULT 2  
US-09-423-863-5  
Sequence 5, Application US/09423863  
Publication No. US20030054336A1  
GENERAL INFORMATION:  
APPLICANT: Donie, Frederic  
APPLICANT: Faatz, Elke  
APPLICANT: Hoess, Eva  
TITLE OF INVENTION: PROCESS FOR THE DETECTION OF HIV ANTIBODIES AND  
FILE REFERENCE: BMID 9974 4638/OP/US-Sz  
CURRENT APPLICATION NUMBER: US/09/423,863  
CURRENT FILING DATE: 2000-02-08  
EARLIER APPLICATION NUMBER: DE 19720914.9  
EARLIER FILING DATE: 1997-05-16  
EARLIER APPLICATION NUMBER: PCT/EP98/02816  
EARLIER FILING DATE: 1998-05-13  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 5  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Human immunodeficiency virus type 1  
US-09-423-863-5

Query Match 59.6%; Score 53; DB 9; Length 16;

Best Local Similarity 60.0%; Pred. No. 0.078;  
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 1 LNSWCKGRHICTY 15  
DB 1 LGIWGSGRHICTT 15

RESULT 3  
US-09-423-863-4  
Sequence 4, Application US/09423863  
Publication No. US20030054336A1  
GENERAL INFORMATION:  
APPLICANT: Donie, Frederic  
APPLICANT: Faatz, Elke  
APPLICANT: Hoess, Eva  
TITLE OF INVENTION: PROCESS FOR THE DETECTION OF HIV ANTIBODIES AND  
FILE REFERENCE: BMID 9974 4638/OP/US-Sz  
CURRENT APPLICATION NUMBER: US/09/423,863  
CURRENT FILING DATE: 2000-02-08  
EARLIER APPLICATION NUMBER: DE 19720914.9  
EARLIER FILING DATE: 1997-05-16  
EARLIER APPLICATION NUMBER: PCT/EP98/02816  
EARLIER FILING DATE: 1998-05-13  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 4  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Human immunodeficiency virus type 1  
US-09-423-863-4

Query Match 58.4%; Score 52; DB 9; Length 16;  
Best Local Similarity 64.3%; Pred. No. 0.11;  
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DB 1 LGIWGSGRHICTT 14

RESULT 4  
US-09-845-042-23  
Sequence 23, Application US/09845042  
Publication No. US20030092177A1  
GENERAL INFORMATION:  
APPLICANT: BELARDELLI, FILIPPO  
APPLICANT: SANTINI, STEFANO MARIA  
APPLICANT: PARLATO, STEFANIA  
APPLICANT: DI PUCCHIO, TIZIANA  
APPLICANT: LOGOZZI, MARIANTONIA  
APPLICANT: LAPENTA, CATERINA  
APPLICANT: FERRANTINI, MARIA  
APPLICANT: SANTODONATO, LORA  
TITLE OF INVENTION: METHOD FOR GENERATING HIGHLY ACTIVE HUMAN DENDRITIC  
CELLS FROM MONOCYTES  
FILE REFERENCE: 618742-8/JP-B-4161  
CURRENT APPLICATION NUMBER: US/09/845,042  
CURRENT FILING DATE: 2001-04-27  
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SOFTWARE: PatentIn Ver. 2.1  
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LENGTH: 21  
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US-09-845-042-23

Query Match 57.3%; Score 51; DB 9; Length 21;  
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Db 10 LGIMCSCGKHLIC 21

US-09-423-863-3  
RESULT 5  
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Publication No. US20030054336A1  
GENERAL INFORMATION:

APPLICANT: Donle, Frederic  
APPLICANT: Faatz, Elke

APPLICANT: Hoess, Eva

TITLE OF INVENTION: PROCESS FOR THE DETECTION OF HIV ANTIBODIES AND

FILE REFERENCE: BMID 9974 4638/OP/US-S2

CURRENT APPLICATION NUMBER: US/09/423.863

EARLIER FILING DATE: 2000-02-08

EARLIER FILING DATE: 1997-05-16

EARLIER APPLICATION NUMBER: PCT/EP98/02816

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 3

LENGTH: 16

TYPE: PRT

ORGANISM: Human Immunodeficiency virus type 1

US-09-423-863-3

Query Match 56.2%; Score 50; DB 9; Length 16;  
Best Local Similarity 53.3%; Pred. No. 0.23;  
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 1 LNSWCGKGRITC 15  
1 ||| |||  
Db 1 LGIMCSCGKHLIC 15

US-09-423-863-6  
RESULT 6

Sequence 6, Application US/09423863

Publication No. US20030054336A1

GENERAL INFORMATION:

APPLICANT: Donle, Frederic

APPLICANT: Faatz, Elke

APPLICANT: Hoess, Eva

TITLE OF INVENTION: PROCESS FOR THE DETECTION OF HIV ANTIBODIES AND

FILE REFERENCE: BMID 9974 4638/OP/US-S2

CURRENT APPLICATION NUMBER: US/09/423.863

EARLIER FILING DATE: 2000-02-08

EARLIER FILING DATE: 1997-05-16

EARLIER APPLICATION NUMBER: PCT/EP98/02816

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 6

LENGTH: 16

TYPE: PRT

ORGANISM: Human Immunodeficiency virus type 1

US-09-423-863-6

Query Match 56.2%; Score 50; DB 9; Length 16;  
Best Local Similarity 53.3%; Pred. No. 0.23;  
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 1 LNSWCGKGRITC 15  
1 ||| |||  
Db 1 LGIMCSCGKHLIC 15

US-09-839-666-10  
RESULT 7

Sequence 10, Application US/09839666

Patent No. US20020025513A1

GENERAL INFORMATION:

APPLICANT: SALBERG, MATTI

TITLE OF INVENTION: ANTIGEN/ANTIBODY SPECIFICITY

EXCHANGER

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: DARBY & DARBY PC

STREET: 805 Third Avenue

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

OPERATING SYSTEM: IBM Compatible

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/839,666

FILING DATE: 19-Apr-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/737,085

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Green, Reza

REGISTRATION NUMBER: 38,475

REFERENCE/DOCKET NUMBER: 3846/OC569

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-527-7659

TELEFAX: 212-753-6237

TELEX: 236687

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 10:

US-09-839-666-10

US-09-423-863-1  
RESULT 8

Sequence 1, Application US/09423863

Publication No. US20030054336A1

GENERAL INFORMATION:

APPLICANT: Donle, Frederic

APPLICANT: Faatz, Elke

APPLICANT: Hoess, Eva

TITLE OF INVENTION: PROCESS FOR THE DETECTION OF HIV ANTIBODIES AND

FILE REFERENCE: BMID 9974 4638/OP/US-S2

CURRENT APPLICATION NUMBER: US/09/423.863

EARLIER FILING DATE: 2000-02-08

EARLIER FILING DATE: 1997-05-16

EARLIER APPLICATION NUMBER: PCT/EP98/02816

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 1

LENGTH: 16

TYPE: PRT

ORGANISM: Human Immunodeficiency virus type 1

US-09-423-863-1

Query Match 55.1%; Score 49; DB 10; Length 10;  
Best Local Similarity 66.7%; Pred. No. 0.21;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 WCGSKRLIC 12  
1 ||| |||  
Db 1 WCGSKRLIC 9

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;; SOFTWARE: Patentin Ver. 2.1
;; SEQ ID NO 1
;; LENGTH: 16
;; TYPE: PRT
;; ORGANISM: Human immunodeficiency virus type 1
US-09-423-863-1
Query Match      55.1%; Score 49; DB 9; Length 16;
Best Local Similarity 57.1%; Pred. No. 0.32;
Matches      8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
OY      1 INSMGCKGRITCT 14
        1 1111111111111111
        1 LGIMGCSGKRICTT 14
        1 LGIMGCSGKRICTT 14
Db
RESULT 9
US-09-388-847-1
; Sequence 1, Application US/09388847
; Publication No. US20030004320A1
; GENERAL INFORMATION:
; APPLICANT: Annunzio, Michael E
; Palumbo, Paul S
; TITLE OF INVENTION: Activated Peptides and Conjugates
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESS: Hoechst Celanese Corporation
; STREET: Route 202-206, P. O. Box 2500
; CITY: Somerville
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08876-1258
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Dell 4100/MXV (IBM PC compatible)
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect for Windows, Version #6.0a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/388,847
; FILING DATE: 02-Sep-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,546
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Rosenstock, Jerome
; REGISTRATION NUMBER: 25,456
; REFERENCE/DOCKET NUMBER: BDI1005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 231-2125
; TELEFAX: (908) 231-4919
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-388-847-1
Query Match      47.2%; Score 42; DB 9; Length 17;
Best Local Similarity 54.5%; Pred. No. 4.1;
Matches      6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
OY      5 GCKGRITCT 15
        1 1111111111111111
        1 GCSGKLICTTA 11
        1 GCSGKLICTTA 11
Db
RESULT 10
US-08-821-739A-78
; Sequence 78, Application US/08821739A
; Patent No. US20020168374A1
```

```
;; GENERAL INFORMATION:
;; APPLICANT: Kudo, Ralph T.
;; APPLICANT: Grey, Howard M.
;; APPLICANT: Sette, Alessandro
;; APPLICANT: Cells, Esteban
;; TITLE OF INVENTION: HIV Binding Peptides and their Uses
;; FILE REFERENCE: 2060.005000A
;; CURRENT APPLICATION NUMBER: US/08/821,739A
;; CURRENT FILING DATE: 1999-03-20
;; PRIOR APPLICATION NUMBER: 60/013,833
;; PRIOR FILING DATE: 1996-03-21
;; PRIOR APPLICATION NUMBER: 08/589,107
;; PRIOR FILING DATE: 1996-07-12
;; PRIOR APPLICATION NUMBER: 08/451,913
;; PRIOR FILING DATE: 1995-05-26
;; PRIOR APPLICATION NUMBER: 08/347,610
;; PRIOR FILING DATE: 1994-12-01
;; PRIOR APPLICATION NUMBER: 08/186,266
;; PRIOR FILING DATE: 1994-01-25
;; PRIOR APPLICATION NUMBER: 08/159,339
;; PRIOR FILING DATE: 1993-11-29
;; PRIOR APPLICATION NUMBER: 08/103,396
;; PRIOR FILING DATE: 1993-08-06
;; PRIOR APPLICATION NUMBER: 08/027,746
;; PRIOR FILING DATE: 1993-03-05
;; PRIOR APPLICATION NUMBER: 07/926,666
;; PRIOR FILING DATE: 1992-08-07
;; NUMBER OF SEQ ID NOS: 149
;; SOFTWARE: Patentin version 3.1
;; SEQ ID NO 78
;; TYPE: PRT
;; LENGTH: 9
;; ORGANISM: Homo sapiens
US-08-821-739A-78
Query Match      44.9%; Score 40; DB 1; Length 9;
Best Local Similarity 62.5%; Pred. No. 3.5e+05;
Matches      5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
OY      4 WCKGRIT 11
        1 111111111
        2 WCKSGKLI 9
        2 WCKSGKLI 9
Db
RESULT 11
US-09-894-018-80
; Sequence 80, Application US/09894018
; Patent No. US20020119127A1
; GENERAL INFORMATION:
; APPLICANT: EPIMUNE, Inc.
; APPLICANT: Sette, Alessandro
; APPLICANT: Chestnut, Robert
; APPLICANT: Livingston, Brian
; APPLICANT: Baker, Dennis
; APPLICANT: Newman, Mark
; APPLICANT: Brown, David
; TITLE OF INVENTION: METHODS AND SYSTEM FOR OPTIMIZING
; MINIGENES AND PEPTIDES THEREBY
; FILE REFERENCE: 39963-2003.00
; CURRENT APPLICATION NUMBER: US/09/894,018
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: PCT/US00/35568
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/173,390
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: US 60/284,221
; PRIOR FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 80
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
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FEATURE:  
OTHER INFORMATION: Oligopeptide  
US-09-894-018-80

Query Match  
Best Local Similarity 44.9%; Score 40; DB 10; Length 9;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 WCGCKRIT 11  
DB 2 WCGCKRIT 9

RESULT 12  
US-09-894-018-185  
Sequence 185, Application US/09894018  
Patent No. US20020119127A1  
GENERAL INFORMATION:  
APPLICANT: EPIMUNE, Inc.  
APPLICANT: Sette, Alessandro  
APPLICANT: Chestnut, Robert  
APPLICANT: Livingston, Brian  
APPLICANT: Baker, Dennis  
APPLICANT: Newman, Mark  
TITLE OF INVENTION: METHODS AND SYSTEM FOR OPTIMIZING  
FILE REFERENCE: 39963-2003.00  
CURRENT APPLICATION NUMBER: US/09/894,018  
PRIOR FILING DATE: 2001-06-27  
PRIOR APPLICATION NUMBER: PCT/US00/35568  
PRIOR FILING DATE: 2000-12-28  
PRIOR APPLICATION NUMBER: US 60/173,390  
PRIOR FILING DATE: 1999-12-28  
PRIOR APPLICATION NUMBER: US 60/284,221  
NUMBER OF SEQ ID NOS: 368  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 185  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Transgenic mouse  
US-09-894-018-185

Query Match  
Best Local Similarity 44.9%; Score 40; DB 10; Length 9;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 WCGCKRIT 11  
DB 2 WCGCKRIT 9

RESULT 13  
US-09-765-086-43  
Sequence 43, Application US/09765086  
Patent No. US20010046498A1  
GENERAL INFORMATION:  
APPLICANT: Ruoslahti, Erkki  
APPLICANT: Pasqualini, Renata  
APPLICANT: Wadth, Arap  
APPLICANT: Bredesen, Dale E.  
APPLICANT: Ellerby, H. Michael  
TITLE OF INVENTION: Chimeric Prostate-Homing Peptides With  
FILE REFERENCE: P-LJ 3844  
CURRENT APPLICATION NUMBER: US/09/765,086  
PRIOR FILING DATE: 2001-01-17  
PRIOR APPLICATION NUMBER: US 09/489,582  
NUMBER OF SEQ ID NOS: 235  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 43

LENGTH: 10  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: synthetic peptide  
US-09-765-086-43

Query Match  
Best Local Similarity 41.6%; Score 37; DB 10; Length 10;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 WCGCKR 9  
DB 2 WCGCKR 7

RESULT 14  
US-10-026-741-41  
Sequence 41, Application US/10026741  
Publication No. US20030049604A1  
GENERAL INFORMATION:  
APPLICANT: CHARNEAU, PIERRE  
CLAVEL, FRANCOISE  
BORMAN, ANDREW  
QUILLIENT, CAROLINE  
GUETARD, DENISE  
MONTAGNIER, LUC  
DONON DE SAINT-MARTIN, JACQUELINE  
COHEN, JACQUES  
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF HIV-1 TYPE (OR  
SUBTYPE) ANTIGENS  
NUMBER OF SEQUENCES: 103  
CORRESPONDENCE ADDRESS:  
ADDRESS: Flinnegan, Henderson, Farabow, Garrett &  
Dunnet, L.L.P.  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/026,741  
FILING DATE: 27-Dec-2001  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/817,441  
FILING DATE: 31-Aug-1998  
APPLICATION NUMBER: PCT/FR 95/01391  
FILING DATE: 20-Oct-1995  
APPLICATION NUMBER: FR 9412554  
FILING DATE: 20-Oct-1994  
APPLICATION NUMBER: FR 9502526  
FILING DATE: 03-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 03660, 6005-00000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 41:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 41:  
US-10-026-741-41

Query Match 40.4%; Score 36; DB 9; Length 6;  
Best Local Similarity 83.3%; Pred. No. 3.3e+05;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 WGCGR 9  
1 WGCGR 6

RESULT 15

US-08-821-739A-90  
; Sequence 90, Application US/08821739A  
; Patent No. US20020168374A1  
; GENERAL INFORMATION:  
; APPLICANT: Kubo, Ralph T.  
; APPLICANT: Grey, Howard M.  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Celis, Esteban  
; TITLE OF INVENTION: HLA Binding Peptides and Their Uses  
; FILE REFERENCE: 2060.005000A  
; CURRENT APPLICATION NUMBER: US/08/821,739A  
; PRIOR FILING DATE: 1999-03-20  
; PRIOR APPLICATION NUMBER: 60/013,833  
; PRIOR FILING DATE: 1996-03-21  
; PRIOR APPLICATION NUMBER: 08/589,107  
; PRIOR FILING DATE: 1996-07-12  
; PRIOR APPLICATION NUMBER: 08/451,913  
; PRIOR FILING DATE: 1995-05-26  
; PRIOR APPLICATION NUMBER: 08/347,610  
; PRIOR FILING DATE: 1994-12-01  
; PRIOR APPLICATION NUMBER: 08/186,266  
; PRIOR FILING DATE: 1994-01-25  
; PRIOR APPLICATION NUMBER: 08/159,339  
; PRIOR FILING DATE: 1993-11-29  
; PRIOR APPLICATION NUMBER: 08/103,396  
; PRIOR FILING DATE: 1993-08-06  
; PRIOR APPLICATION NUMBER: 08/027,746  
; PRIOR FILING DATE: 1993-03-05  
; PRIOR APPLICATION NUMBER: 07/926,666  
; PRIOR FILING DATE: 1992-08-07  
; NUMBER OF SEQ ID NOS: 149  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 90  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-08-821-739A-90

Query Match 40.4%; Score 36; DB 1; Length 10;  
Best Local Similarity 55.6%; Pred. No. 21;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 LMSWCGGR 9  
2 LGIWGCGSK 10

RESULT 16  
US-09-910-009A-481  
; Sequence 481, Application US/09910009A  
; Publication No. US20030050234A1  
; GENERAL INFORMATION:  
; APPLICANT: University of Utah Research Foundation  
; APPLICANT: Cognetix, Inc.  
; APPLICANT: Oliveira, Baldomero M.  
; APPLICANT: McIntosh, J. Michael  
; APPLICANT: Garrett, James E.  
; APPLICANT: Watkins, Maren  
; APPLICANT: Cruz, Lourdes J.  
; APPLICANT: Shon, Ki-Joon  
; APPLICANT: Jacobsen, Richard  
; APPLICANT: Jones, Robert M.

APPLICANT: Cartier, G. Edward  
; APPLICANT: Shen, Greg S.  
; APPLICANT: Magstaff, John D.  
; TITLE OF INVENTION: Mu-Conopeptides  
; FILE REFERENCE: 2314-242  
; CURRENT APPLICATION NUMBER: US/09/910,009A  
; PRIOR FILING DATE: 2001-07-23  
; PRIOR APPLICATION NUMBER: US 60/219,619  
; PRIOR FILING DATE: 2000-07-21  
; PRIOR APPLICATION NUMBER: US 60/245,157  
; PRIOR FILING DATE: 2000-11-03  
; PRIOR APPLICATION NUMBER: US 60/264,319  
; PRIOR FILING DATE: 2001-01-29  
; PRIOR APPLICATION NUMBER: US 60/277,270  
; PRIOR FILING DATE: 2001-03-21  
; NUMBER OF SEQ ID NOS: 520  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 481  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Conus ermineus  
US-09-910-009A-481

Query Match 39.3%; Score 35; DB 9; Length 20;  
Best Local Similarity 33.3%; Pred. No. 57;  
Matches 5; Conservative 4; Mismatches 2; Indels 4; Gaps 1;

QY 3 SWGC---KGRITCY 13  
3 SWPCRRISNGKIVCF 17

RESULT 17  
US-10-026-741-5  
; Sequence 5, Application US/10026741  
; Publication No. US20030049604A1  
; GENERAL INFORMATION:  
; APPLICANT: CHARNEAU, PIERRE  
; CLAVEL, FRANCOISE  
; BORMAN, ANDREM  
; OUILLENT, CAROLINE  
; GUETARD, DENISE  
; MONTAGNIER, LUC  
; DONDON DE SAINT-MARTIN, JACQUELINE  
; COHEN, JACQUES  
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF HIV-1 TYPE (OR  
SUBTYPE) ANTIGENS  
; NUMBER OF SEQUENCES: 103  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Flinnegan, Henderson, Farabow, Garrett &  
; Dunner, L.L.P.  
; STREET: 1300 I Street, N.W.  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 20005-3315  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/026,741  
; FILING DATE: 27-Dec-2001  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/817,441  
; FILING DATE: 31-AUG-1998  
; APPLICATION NUMBER: PCT/FR 95/01391  
; FILING DATE: 20-OCT-1995  
; APPLICATION NUMBER: FR 9412554  
; FILING DATE: 20-OCT-1994  
; APPLICATION NUMBER: FR 9502526  
; FILING DATE: 03-MAR-1995

```
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03260, 6005-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-026-741-5

Query Match      38.2% Score 34; DB 9; Length 7;
Best Local Similarity 71.4%; Pred. No. 3.5e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      6 CKGRICYS 12
DB      1 CKNRILC 7

RESULT 18
US-09-423-863-10
Sequence 10, Application US/09423863
Publication No. US20030054336a1
GENERAL INFORMATION:
APPLICANT: Donle, Frederic
APPLICANT: Hoess, Eva
TITLE OF INVENTION: PROCESS FOR THE DETECTION OF HIV ANTIBODIES AND
TITLE OF INVENTION: ANTIGENS USED IN IT
FILE REFERENCE: BMID 9974 4638/OP/US-S2
CURRENT APPLICATION NUMBER: US/09/423,863
CURRENT FILING DATE: 2000-02-08
EARLIER APPLICATION NUMBER: DE 19720914.9
EARLIER FILING DATE: 1997-05-16
EARLIER APPLICATION NUMBER: PCT/EP98/02816
EARLIER FILING DATE: 1998-05-13
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 10
LENGTH: 10
TYPE: PRT
ORGANISM: Human Immunodeficiency virus type 1
US-09-423-863-10

Query Match      38.2% Score 34; DB 9; Length 10;
Best Local Similarity 60.0%; Pred. No. 44;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      6 CKGRICYS 15
DB      1 CSGRHCITN 10

RESULT 19
US-09-423-863-11
Sequence 11, Application US/09423863
Publication No. US20030054336a1
GENERAL INFORMATION:
APPLICANT: Donle, Frederic
APPLICANT: Faatz, Elke
APPLICANT: Hoess, Eva
TITLE OF INVENTION: PROCESS FOR THE DETECTION OF HIV ANTIBODIES AND
TITLE OF INVENTION: ANTIGENS USED IN IT
FILE REFERENCE: BMID 9974 4638/OP/US-S2
CURRENT APPLICATION NUMBER: US/09/423,863
CURRENT FILING DATE: 2000-02-08
```

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EARLIER APPLICATION NUMBER: DE 19720914.9
EARLIER FILING DATE: 1997-05-16
EARLIER APPLICATION NUMBER: PCT/EP98/02816
EARLIER FILING DATE: 1998-05-13
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11
LENGTH: 10
TYPE: PRT
ORGANISM: Human Immunodeficiency virus type 1
US-09-423-863-11

Query Match      38.2% Score 34; DB 9; Length 10;
Best Local Similarity 60.0%; Pred. No. 44;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      6 CKGRICYS 15
DB      1 CSGRHCITN 10

RESULT 20
US-09-423-863-9
Sequence 9, Application US/09423863
Publication No. US20030054336a1
GENERAL INFORMATION:
APPLICANT: Donle, Frederic
APPLICANT: Faatz, Elke
APPLICANT: Hoess, Eva
TITLE OF INVENTION: PROCESS FOR THE DETECTION OF HIV ANTIBODIES AND
TITLE OF INVENTION: ANTIGENS USED IN IT
FILE REFERENCE: BMID 9974 4638/OP/US-S2
CURRENT APPLICATION NUMBER: US/09/423,863
CURRENT FILING DATE: 2000-02-08
EARLIER APPLICATION NUMBER: DE 19720914.9
EARLIER FILING DATE: 1997-05-16
EARLIER APPLICATION NUMBER: PCT/EP98/02816
EARLIER FILING DATE: 1998-05-13
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 9
LENGTH: 10
TYPE: PRT
ORGANISM: Human Immunodeficiency virus type 1
US-09-423-863-9

Query Match      37.1% Score 33; DB 9; Length 10;
Best Local Similarity 66.7%; Pred. No. 62;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      6 CKGRICYS 14
DB      1 CSGRHCITN 9

RESULT 21
US-09-845-612B-14
Sequence 14, Application US/09845612B
Publication No. US20030083261a1
GENERAL INFORMATION:
APPLICANT: YU, HONGTAO
APPLICANT: TANG, ZHANYUN
APPLICANT: LUO, XUELIAN
APPLICANT: RIZO-REY, JOSE
TITLE OF INVENTION: A CLASS OF 12MER PEPTIDES THAT INHIBIT THE FUNCTION OF THE MIT
FILE REFERENCE: UTSD:795
CURRENT APPLICATION NUMBER: US/09/845,612B
CURRENT FILING DATE: 2001-04-27
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.0
SEQ ID NO 14
LENGTH: 15
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TYPE: PRT  
ORGANISM: Drosophila  
US-09-845-612B-14

Query Match  
Best Local Similarity 37.1%; Score 33; DB 9; Length 15;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 GRICCY 13  
111111  
DB 5 GRICCY 10

RESULT 22  
US-09-423-863-8  
Sequence 8, Application US/09423863  
Publication No. US20030054336A1  
GENERAL INFORMATION:  
APPLICANT: Donle, Frederic  
APPLICANT: Faatz, Elke  
APPLICANT: Hoess, Eva  
TITLE OF INVENTION: PROCESS FOR THE DETECTION OF HIV ANTIBODIES AND  
FILE REFERENCE: BMID 9974 4638/OP/US-S2  
CURRENT APPLICATION NUMBER: US/09/423,863  
EARLIER FILING DATE: 2000-02-08  
EARLIER APPLICATION NUMBER: DE 19720914.9  
EARLIER FILING DATE: 1997-05-16  
EARLIER APPLICATION NUMBER: PCT/EP98/02816  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 8  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Human immunodeficiency virus type 1  
US-09-423-863-8

Query Match  
Best Local Similarity 34.8%; Score 31; DB 9; Length 10;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 CCKRITCYTS 15  
11111111  
DB 1 CCKGHICITTN 10

RESULT 23  
US-09-910-009A-416  
Sequence 416, Application US/09910009A  
Publication No. US20030050234A1  
GENERAL INFORMATION:  
APPLICANT: University of Utah Research Foundation  
APPLICANT: Cognetix, Inc.  
APPLICANT: Olivera, Baldomero M.  
APPLICANT: McIntosh, J. Michael  
APPLICANT: Garrett, James E.  
APPLICANT: Watkins, Maren  
APPLICANT: Cruz, Lourdes J.  
APPLICANT: Shon, Ki-Joon  
APPLICANT: Jacobsen, Richard  
APPLICANT: Jones, Robert M.  
APPLICANT: Cartier, G. Edward  
APPLICANT: Shen, Greg S.  
APPLICANT: Magstaff, John D.  
TITLE OF INVENTION: Mu-Conopeptides  
FILE REFERENCE: 2314-242  
CURRENT APPLICATION NUMBER: US/09/910,009A  
EARLIER FILING DATE: 2001-07-23  
EARLIER APPLICATION NUMBER: US 60/219,619  
PRIOR FILING DATE: 2000-07-21  
PRIOR APPLICATION NUMBER: US 60/245,157  
PRIOR FILING DATE: 2000-11-03

PRIOR APPLICATION NUMBER: US 60/264,319  
PRIOR FILING DATE: 2001-01-29  
PRIOR APPLICATION NUMBER: US 60/277,270  
PRIOR FILING DATE: 2001-03-21  
NUMBER OF SEQ ID NOS: 520  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 416  
LENGTH: 13  
TYPE: PRT  
ORGANISM: Conus laterculatus  
US-09-910-009A-416

Query Match  
Best Local Similarity 34.8%; Score 31; DB 9; Length 13;  
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 WCKGRITC 12  
111111  
DB 4 WPCSGCIPC 12

RESULT 24  
US-10-142-238A-49  
Sequence 49, Application US/10142238A  
Publication No. US20030087819A1  
GENERAL INFORMATION:  
APPLICANT: Bielski, John K.  
TITLE OF INVENTION: CYSTEINE-CONTAINING PEPTIDES HAVING OXIDANT PROPERTIES  
FILE REFERENCE: IB-1705  
CURRENT APPLICATION NUMBER: US/10/142,238A  
CURRENT FILING DATE: 2002-08-19  
PRIOR APPLICATION NUMBER: US 60/289,944  
PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 84  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 49  
LENGTH: 18  
TYPE: PRT  
ORGANISM: ARTIFICIAL SEQUENCE  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (1)-(18)  
OTHER INFORMATION: HUMAN GENETIC ORIGIN  
US-10-142-238A-49

Query Match  
Best Local Similarity 34.8%; Score 31; DB 9; Length 18;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 CCKRITCY 13  
1111111  
DB 7 CCKRLVQY 14

RESULT 25  
US-09-423-863-7  
Sequence 7, Application US/09423863  
Publication No. US20030054336A1  
GENERAL INFORMATION:  
APPLICANT: Donle, Frederic  
APPLICANT: Faatz, Elke  
APPLICANT: Hoess, Eva  
TITLE OF INVENTION: PROCESS FOR THE DETECTION OF HIV ANTIBODIES AND  
FILE REFERENCE: BMID 9974 4638/OP/US-S2  
CURRENT APPLICATION NUMBER: US/09/423,863  
CURRENT FILING DATE: 2000-02-08  
EARLIER APPLICATION NUMBER: DE 19720914.9  
EARLIER FILING DATE: 1997-05-16  
EARLIER APPLICATION NUMBER: PCT/EP98/02816  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn Ver. 2.1



SEQ ID NO 7  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Human Immunodeficiency virus type 1  
US-09-423-863-7

Query Match 33.7% Score 30; DB 9; Length 10;  
Best Local Similarity 55.6% Pred. No. 1.8e+02;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
CY 6 CKGRHICT 14  
DB 1 CKGRHICT 9

RESULT 26  
US-09-572-404B-922  
Sequence 922, Application US/09572404B  
Publication No. US20030078374A1  
GENERAL INFORMATION:  
APPLICANT: Proteom Ltd  
TITLE OF INVENTION: Complementary peptide ligands from the human genome  
FILE REFERENCE: Human patent  
CURRENT APPLICATION NUMBER: US/09/572,404B  
CURRENT FILING DATE: 2000-05-17  
NUMBER OF SEQ ID NOS: 4203  
SOFTWARE: ProPatent version 1.0  
SEQ ID NO 922  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Homo Sapiens  
FEATURE:  
OTHER INFORMATION: sequence located in MPPA at 11-20 and may interact with sequence  
US-09-572-404B-922

Query Match 33.7% Score 30; DB 9; Length 10;  
Best Local Similarity 100.0% Pred. No. 1.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SWGC 6  
DB 7 SWGC 10

RESULT 27  
US-09-969-192-68

Sequence 68, Application US/09569192  
Patent No. US20020151027A1  
GENERAL INFORMATION:  
APPLICANT: WICKHAM, THOMAS J.  
ROELVINK, PETRUS W.

TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF  
CONSTRAINED PEPTIDE MOTIFS  
NUMBER OF SEQUENCES: 80  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Leydig, Volt & Mayer, Ltd.  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60601

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/969,192  
FILING DATE: 01-Oct-2001  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 9-455061

FILING DATE: 06-DEC-1999  
APPLICATION NUMBER: US 9-130225  
FILING DATE: 06-AUG-1998  
APPLICATION NUMBER: US 8-701124  
FILING DATE: 21-AUG-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Heftner, M. Daniel  
REGISTRATION NUMBER: 41,826  
REFERENCE/DOCKET NUMBER: 213564  
INFORMATION FOR SEQ ID NO: 68:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
MOLECULE TYPE: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 68:  
US-09-969-192-68

Query Match 33.7% Score 30; DB 10; Length 14;  
Best Local Similarity 50.0% Pred. No. 2.5e+02;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 6 CKGRHICTS 15  
DB 5 CKGRHICTS 14

RESULT 28  
US-09-974-879-281  
Sequence 281, Application US/09974879  
Publication No. US20030028003A1  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: 125 Human Secreted Proteins  
FILE REFERENCE: P020P2  
CURRENT APPLICATION NUMBER: US/09/974,879  
CURRENT FILING DATE: 2001-10-12  
PRIOR APPLICATION NUMBER: US 60/239,893  
PRIOR FILING DATE: 2000-10-13  
PRIOR APPLICATION NUMBER: US 09/818,683  
PRIOR FILING DATE: 2001-03-28  
PRIOR APPLICATION NUMBER: US 09/305,736  
PRIOR FILING DATE: 1999-05-05  
PRIOR APPLICATION NUMBER: PCT/US98/23435  
PRIOR FILING DATE: 1998-11-04  
PRIOR APPLICATION NUMBER: US 60/064,911  
PRIOR FILING DATE: 1997-11-07  
PRIOR APPLICATION NUMBER: US 60/064,912  
PRIOR FILING DATE: 1997-11-07  
PRIOR APPLICATION NUMBER: US 60/064,983  
PRIOR FILING DATE: 1997-11-07  
PRIOR APPLICATION NUMBER: US 60/064,900  
PRIOR FILING DATE: 1997-11-07  
PRIOR APPLICATION NUMBER: US 60/064,988  
PRIOR FILING DATE: 1997-11-07  
PRIOR APPLICATION NUMBER: US 60/064,987  
PRIOR FILING DATE: 1997-11-07  
PRIOR APPLICATION NUMBER: US 60/064,908  
PRIOR FILING DATE: 1997-11-07  
PRIOR APPLICATION NUMBER: US 60/064,984  
PRIOR FILING DATE: 1997-11-07  
PRIOR APPLICATION NUMBER: US 60/064,985  
PRIOR FILING DATE: 1997-11-07  
PRIOR APPLICATION NUMBER: US 60/066,094  
PRIOR FILING DATE: 1997-11-17  
PRIOR APPLICATION NUMBER: US 60/066,100  
PRIOR FILING DATE: 1997-11-17  
PRIOR APPLICATION NUMBER: US 60/066,089  
PRIOR FILING DATE: 1997-11-17  
PRIOR APPLICATION NUMBER: US 60/066,095  
PRIOR FILING DATE: 1997-11-17  
PRIOR APPLICATION NUMBER: US 60/066,090

PRIOR FILING DATE: 1997-11-17  
NUMBER OF SEQ ID NOS: 611  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 281  
LENGTH: 21  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-974-879-281

Query Match 33.7%: Score 30; DB 9; Length 21;  
Best Local Similarity 71.4%: Pred. No. 3.5e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 LNSMGCK 7  
| | | | |  
DB 10 LRSWGAK 16

RESULT 29  
US-09-305-736-269  
Sequence 269, Application US/09305736  
Publication No. US20030086078A1  
GENERAL INFORMATION:  
APPLICANT: Feng et al.  
TITLE OF INVENTION: 125 Human Secreted Proteins  
FILE REFERENCE: P2020P1  
CURRENT APPLICATION NUMBER: US/09/305,736  
CURRENT FILING DATE: 1999-05-05  
EARLIER APPLICATION NUMBER: PCT/US98/23435  
EARLIER FILING DATE: 1998-11-04  
EARLIER APPLICATION NUMBER: 60/064,911  
EARLIER FILING DATE: 1997-11-07  
EARLIER APPLICATION NUMBER: 60/064,912  
EARLIER FILING DATE: 1997-11-07  
EARLIER APPLICATION NUMBER: 60/064,983  
EARLIER FILING DATE: 1997-11-07  
EARLIER APPLICATION NUMBER: 60/064,900  
EARLIER FILING DATE: 1997-11-07  
EARLIER APPLICATION NUMBER: 60/064,988  
EARLIER FILING DATE: 1997-11-07  
EARLIER APPLICATION NUMBER: 60/064,987  
EARLIER FILING DATE: 1997-11-07  
EARLIER APPLICATION NUMBER: 60/064,908  
EARLIER FILING DATE: 1997-11-07  
EARLIER APPLICATION NUMBER: 60/064,984  
EARLIER FILING DATE: 1997-11-07  
EARLIER APPLICATION NUMBER: 60/064,985  
EARLIER FILING DATE: 1997-11-07  
EARLIER APPLICATION NUMBER: 60/066,094  
EARLIER FILING DATE: 1997-11-17  
EARLIER APPLICATION NUMBER: 60/066,100  
EARLIER FILING DATE: 1997-11-17  
EARLIER APPLICATION NUMBER: 60/066,089  
EARLIER FILING DATE: 1997-11-17  
EARLIER APPLICATION NUMBER: 60,066,095  
EARLIER FILING DATE: 1997-11-17  
EARLIER APPLICATION NUMBER: 60/066,090  
EARLIER FILING DATE: 1997-11-17  
NUMBER OF SEQ ID NOS: 612  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 269  
LENGTH: 21  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-305-736-269

Query Match 33.7%: Score 30; DB 9; Length 21;  
Best Local Similarity 71.4%: Pred. No. 3.5e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 LNSMGCK 7  
| | | | |  
DB 10 LRSWGAK 16

RESULT 30  
US-09-999-724-93  
Sequence 93, Application US/09999724  
Publication No. US20030022355A1  
GENERAL INFORMATION:  
APPLICANT: WICKHAM, THOMAS J.  
APPLICANT: KOVESDI, IMRE  
APPLICANT: BROUGH, DOUGLAS E.  
TITLE OF INVENTION: VECTORS AND METHODS FOR GENE TRANSFER  
FILE REFERENCE: 212960  
CURRENT APPLICATION NUMBER: US/09/999,724  
CURRENT FILING DATE: 2001-10-24  
PRIOR APPLICATION NUMBER: US 09/101,751  
PRIOR FILING DATE: 1999-01-29  
PRIOR APPLICATION NUMBER: WO 96US19150  
PRIOR FILING DATE: 1996-11-27  
PRIOR APPLICATION NUMBER: US 08/700,846  
PRIOR FILING DATE: 1996-08-21  
PRIOR APPLICATION NUMBER: US 08/701,124  
PRIOR FILING DATE: 1996-08-21  
PRIOR APPLICATION NUMBER: US 08/563,368  
PRIOR FILING DATE: 1995-11-28  
NUMBER OF SEQ ID NOS: 94  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 93  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic  
US-09-999-724-93

Query Match 32.6%: Score 29; DB 9; Length 14;  
Best Local Similarity 50.0%: Pred. No. 3.5e+02;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 6 CKGRILCYTS 15  
| : | | | |  
DB 5 CRGDFCGTS 14

Search completed: June 5, 2003, 07:27:41  
Job time : 230 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 5, 2003, 08:58:43 ; Search time 15 Seconds

(without alignments)  
96.134 Million cell updates/sec

Title: US-09-605-573A-69\_COPY\_12\_26

Perfect score: 89

Sequence: 1 LNSWGCKGRICYS 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

PIR\_73:\*\*  
1: PIR1:\*\*  
2: PIR2:\*\*  
3: PIR3:\*\*  
4: PIR4:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	30.3	13	2	S57567
2	27	30.3	20	2	S29635
3	26.5	29.8	15	2	S10386
4	26	29.2	16	2	PC4416
5	26	29.2	19	1	EMSGAN
6	25.5	28.7	17	2	S24570
7	25.5	28.7	19	2	A58700
8	25	28.1	14	2	PH1306
9	25	28.1	15	2	S02381
10	24.5	27.5	10	2	S03530
11	24	27.0	10	2	A59173
12	24	27.0	15	2	PH1318
13	24	27.0	19	2	PK0062
14	23.5	26.4	16	2	S03532
15	23.5	26.4	16	2	D49021
16	23	25.8	7	2	S57274
17	23	25.8	11	2	PH1343
18	23	25.8	12	2	I46922
19	23	25.8	14	2	PH1639
20	23	25.8	15	2	A56786
21	23	25.8	15	2	A45103
22	23	25.8	16	2	A59046
23	23	25.8	18	2	S43958
24	23	25.8	19	2	S43958
25	22.5	25.3	17	2	S03531
26	22	24.7	6	2	A61068
27	22	24.7	8	2	JS0315
28	22	24.7	8	2	JS0316
29	22	24.7	8	2	JS0317

30	22	24.7	9	2	A24244	adipokinetic hormo
31	22	24.7	11	2	A34662	Achatin cardio-ex
32	22	24.7	12	2	S26553	T-cell receptor be
33	22	24.7	12	2	S26548	T-cell receptor be
34	22	24.7	13	2	A61514	glutathione transf
35	22	24.7	15	2	PH1619	Ig H chain V-D-J r
36	22	24.7	16	2	PH1634	Ig H chain V-D-J r
37	22	24.7	17	2	A37823	dihydrolipeamide S
38	22	24.7	18	2	S33645	hypothetical prote
39	22	24.7	19	2	I52623	hypothetical prote
40	22	24.7	19	2	S62864	toxin VI - Rlyus
41	22	24.7	19	2	PH1756	T cell receptor al
42	22	24.7	8	2	US0318	leucokinin VIII -
43	22	24.7	10	2	S51912	hemagglutinin - in
44	22	24.7	10	2	PH0923	T-cell receptor be
45	22	24.7	12	2	S53789	neuropeptide Rec-H
46	22	24.7	13	2	PH1635	Ig H chain V-D-J r
47	22	24.7	13	2	S36668	hypothetical prote
48	22	24.7	14	2	PH0747	T-cell receptor prote
49	22	24.7	17	2	I57941	beta 3-adrenergic
50	22	24.7	17	2	A36824	tachyplestin I - ho
51	22	24.7	17	2	JX0125	Ig heavy chain J r
52	22	24.7	17	2	S03533	Ig heavy chain J r
53	22	24.7	17	2	PS0384	gamma-crystallin I
54	22	24.7	18	2	H75063	gamma-crystallin I
55	22	24.7	19	2	B60894	serine proteinase
56	22	24.7	19	2	JX0124	Ig heavy chain D r
57	22	24.7	19	2	S12268	Ig heavy chain J r
58	22	24.7	20	2	C61570	T-cell receptor be
59	22	24.7	20	2	PC2084	T antigen variant
60	22	24.7	20	2	PH1341	Ig H chain V-D-J r
61	22	24.7	15	2	S10383	somatostatin - sll
62	20.5	23.0	16	2	PS0383	somatostatin I - c
63	20	22.5	9	2	PH0942	somatostatin I - E
64	20	22.5	11	2	PH1375	somatostatin I - s
65	20	22.5	11	2	PH1376	nitrogenase (EC 1.
66	20	22.5	13	2	PH1599	Ig H chain V-D-J r
67	20	22.5	14	2	C60414	Ig H chain V-D-J r
68	20	22.5	14	2	B60842	Ig heavy chain CDR
69	20	22.5	14	2	A60622	Ig H chain V-D-J r
70	20	22.5	14	2	A60840	hypothetical TCR3/
71	20	22.5	14	2	S00172	hypothetical prote
72	20	22.5	14	2	I39753	N-(beta-N-acetylgl
73	20	22.5	14	2	PH1628	ribosomal protein
74	20	22.5	16	2	PM0296	Ig heavy chain CDR
75	20	22.5	16	2	PH1640	probable flagellar
76	20	22.5	16	4	I79565	gamma-crystallin V
77	20	22.5	16	4	A33171	lipoprotein Acqf P
78	20	22.5	18	2	S04229	monocyte chemotact
79	20	22.5	19	2	S49026	Ig heavy chain V r
80	20	22.5	19	2	PM0244	Ig heavy chain J1
81	20	22.5	19	2	A61144	T-cell receptor ga
82	20	22.5	20	2	D60894	isotocin - common
83	20	22.5	20	2	B39108	T-cell receptor be
84	20	22.5	20	2	I67551	T-cell receptor be
85	20	22.5	15	2	S26791	glutathione transf
86	19.5	21.9	18	2	S03528	glucan endo-1,3-be
87	19	21.3	8	2	A38887	T-cell receptor de
88	19	21.3	9	2	A61364	Ig H chain V-D-J r
89	19	21.3	9	2	PT0562	collecting duct wa
90	19	21.3	9	2	S71868	glyceroldehyde-3-p
91	19	21.3	10	2	A53709	leucotoxin III -
92	19	21.3	12	1	S28215	T-cell receptor al
93	19	21.3	12	2	B49033	leucokinin VIII -
94	19	21.3	12	2	PH1587	hemagglutinin - in
95	19	21.3	12	2	B28810	T-cell receptor be
96	19	21.3	13	2	I51905	neuropeptide Rec-H
97	19	21.3	13	2	S54344	Ig H chain V-D-J r
98	19	21.3	14	2	A48389	hypothetical prote
99	19	21.3	14	2	PH0779	hypothetical prote
100	19	21.3	15	2		

## ALIGNMENTS

## RESULT 1

T cell receptor V-J junctional alpha chain region - human (fragment)  
S57567  
C:Species: Homo sapiens (man)  
C:Date: 19-Oct-1995 #sequence\_revision 17-Nov-1995 #text\_change 05-Nov-1999  
C:Accession: S57567  
R:Burrows, S.R.; Sillins, S.L.; Moss, D.J.; Khanna, R.; Misko, I.S.; Argact, V.P.  
Submitted to: The EMBL Data Library, June 1995  
A:Description: T cell receptor repertoire for a viral epitope in humans is diversified  
A:Reference number: S57494  
A:Accession: S57567  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-13 <BUR>  
A:Cross-references: EMBL:Z49949; NID:9887470; PIDN:CAA90220.1; PID:9887471  
C:Keywords: T-cell receptor

Query Match 30.3%; Score 27; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 6.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 NSMG 5  
Db 5 NSMG 8

## RESULT 2

jacalin beta chain - Artocarpus tonkinensis  
S29635  
C:Species: Artocarpus tonkinensis  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 24-Jul-1997  
C:Accession: S29635  
R:Ngoc, L.D.; Brillard, M.; Hoebeke, J.  
Biochim. Biophys. Acta 1156, 219-222, 1993  
A:Title: The alpha- and beta-subunits of the jacalins are cleavage products from a 17-kD  
A:Reference number: S29635; MUID:93152601; PMID:8427879  
A:Accession: S29635  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-20 <NGO>

Query Match 30.3%; Score 27; DB 2; Length 20;  
Best Local Similarity 57.1%; Pred. No. 9.1e+02;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 LNSMGCK 7  
Db 12 VGSWGAK 18

## RESULT 3

Ig heavy chain J region (clone Re107) - little skate (fragment)  
S10386  
C:Species: Raja erinacea (little skate)  
C:Date: 30-Jun-1991 #sequence\_revision 30-Jun-1991 #text\_change 16-Aug-1996  
C:Accession: S10386  
R:Harding, F.A.; Cohen, N.; Litman, G.W.  
Nucleic Acids Res. 18, 1015-1020, 1990  
A:Title: Immunoglobulin heavy chain gene organization and complexity in the skate, Raja  
A:Reference number: S08462; MUID:90192082; PMID:2107524  
A:Accession: S10386  
A:Molecule type: DNA  
A:Residues: 1-15 <HAK>  
A:Cross-references: EMBL:X15124  
C:Keywords: heterotetramer; immunoglobulin

Query Match 29.8%; Score 26.5; DB 2; Length 15;  
Best Local Similarity 40.0%; Pred. No. 8.6e+02;  
Matches 6; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

OY 1 LNSMGCKRIICYS 15  
Db 2 LDYWG-ESTWTVTS 15

## RESULT 4

PC4416  
ErbB kinase activator gamma, brain and thymus - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 10-Dec-1997 #sequence\_revision 10-Dec-1997 #text\_change 02-Aug-2002  
C:Accession: PC4416  
R:Hisashiyama, S.; Horikawa, M.; Yamada, K.; Ichino, N.; Nakano, N.; Nakagawa, T.; Mi  
J. Biochem. 122, 675-680, 1997  
A:Title: A novel brain-derived member of the epidermal growth factor family that inte  
A:Reference number: J05700; MUID:98006324; PMID:9348101  
A:Accession: PC4416  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-16 <HIG>  
A:Cross-references: DBJ:D89998; NID:92605635; PIDN:BAA23347.1; PID:92605636  
A:Experimental source: PC-12 cell  
A:Comment: This protein is a member of the epidermal growth factor family. It is func  
ating the differentiation of MDA-MB-453 cells.  
C:Superfamily: human ErbB kinase activator alpha, brain and thymus; EGF homology

Query Match 29.2%; Score 26; DB 2; Length 16;  
Best Local Similarity 50.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 LNSMGCKG 8  
Db 9 INOLSCKG 16

## RESULT 5

EMSMAN  
ancovenin - Streptomyces sp. (strain A647P-2)  
C:Species: Streptomyces sp.  
C:Date: 12-May-1994 #sequence\_revision 19-May-1994 #text\_change 19-May-1994  
C:Accession: A61284  
R:Nakamiya, T.; Ueki, Y.; Shiba, T.; Kido, Y.; Motoki, Y.  
Tetrahedron Lett. 26, 665-668, 1985  
A:Title: The structure of ancovenin, a new peptide inhibitor of angiotensin I convert  
A:Reference number: A61284  
A:Accession: A61284  
A:Molecule type: protein  
A:Residues: 1-19 <NAK>  
C:Superfamily: cinnamycin precursor  
C:Keywords: antibiotic; lanthionine  
F:1-18/Cross-link: (2S,3S,6R)-3-methyl-lanthionine (Cys-Thr) #status experimental  
F:4-14/Cross-link: sn-(2S,6R)-lanthionine (Ser-Cys) #status experimental  
F:5-11/Cross-link: (2S,3S,6R)-3-methyl-lanthionine (Cys-Thr) #status experimental  
F:6/Modified site: dehydroalanine (Ser) #status experimental

Query Match 29.2%; Score 26; DB 1; Length 19;  
Best Local Similarity 50.0%; Pred. No. 1.2e+03;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 3 SMGCKG 8  
Db 11 TWSCDG 16

## RESULT 6

S24570  
Ig heavy chain J region - channel catfish  
C:Species: Ictalurus punctatus (channel catfish)  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Jul-1999  
C:Accession: S24570  
R:Wilson, M.R.  
Submitted to the EMBL Data Library, March 1992  
A:Reference number: S24570  
A:Accession: S24570

A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-17 <MIL>  
A:Cross-references: EMBL:X65182; NID:964015; PIRN:CMA46293.1; PID:964016  
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology  
C:Keywords: heterotetramer; Immunoglobulin

Query Match 28.7% Score 25.5; DB 2; Length 17;  
Best Local Similarity 50.0%; Pred. No. 1.4e+03;  
Matches 6; Conservative 1; Mismatches 4; Indels 1; Gaps 1;  
OY 4 WCKGRICTYS 15  
DB 7 WG-KGTAVTVTS 17

RESULT 7  
A58700  
actgardine [validated] - "Actinoplanes liguriae"  
N:Alternate names: gardimycin  
C:Species: "Actinoplanes liguriae"  
A:Note: ATCC 31048

C:Date: 16-Jan-1998 #sequence\_revision 23-Jan-1998 #text\_change 15-Sep-2000  
C:Accession: A58700; A58701  
R:Zimmermann, N.; Jung, G.  
Eur. J. Biochem. 246, 809-819, 1997  
A:Title: The three-dimensional solution structure of the lantibiotic murein-biosynthesis  
A:Reference number: A58700; MUID:97363218; PMID:9219543  
A:Accession: A58700  
A:Molecule type: protein  
A:Residues: 1-19 <ZYM>  
A:Note: the assignment of residues 1-Ser and 6-Cys are based on model studies  
R:Zimmermann, N.; Metzger, J.W.; Jung, G.  
Eur. J. Biochem. 228, 786-797, 1995  
A:Title: The tetracyclic lantibiotic actegardine. (1)H-NMR and (13)C-NMR assignments and  
A:Reference number: A58701; MUID:9555286; PMID:7737178  
A:Accession: A58701  
A:Molecule type: protein  
A:Residues: 'X',2-5,'X',7-19 <Z12>  
A:Note: residues 1 and 6, indicated as 'X', are serine and cysteine, but which is in whi  
R:Zimmermann, N.; Jung, G.  
submitted to the Brookhaven Protein Data Bank, May 1997  
A:Reference number: A67976; PDB:1AJ1  
A:Content: annotation, conformation and cross-link assignments by (1)H- and (13)C-NMR,  
C:Superfamily: unassigned lantibiotic-containing peptides  
C:Keywords: antibiotic; lantibiotic  
F:1-6/Cross-link: sn-(2S,6R)-lanthionine (Ser-Cys) #status experimental  
F:7-12/Cross-link: (2S,3S,6R)-3-methyl-lanthionine (Thr-Cys) #status experimental  
F:9-17/Cross-link: (2S,3S,6R)-3-methyl-lanthionine (Thr-Cys) #status experimental  
F:14-19/Cross-link: (2S,3S,6R)-3-methyl-lanthionine (Thr-Cys) #status experimental

Query Match 28.7% Score 25.5; DB 2; Length 19;  
Best Local Similarity 31.2%; Pred. No. 1.5e+03;  
Matches 5; Conservative 2; Mismatches 4; Indels 5; Gaps 1;  
OY 2 NSMGCK-----GRITC 12  
DB 2 SGWVCTLTIECTVIC 17

RESULT 8  
PH1306  
Ig heavy chain DJ region (clone C96-100) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C:Accession: PH1306  
R:Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.  
J. Exp. Med. 176, 1577-1581, 1992  
A:Title: Predominance of fetal type DJH joining in young children with B precursor lymph  
A:Reference number: PH1302; MUID:95094761; PMID:1460419  
A:Accession: PH1306  
A:Molecule type: DNA

A:Residues: 1-14 <MAS>  
C:Keywords: heterotetramer; Immunoglobulin

Query Match 28.1% Score 25; DB 2; Length 14;  
Best Local Similarity 60.0%; Pred. No. 1.4e+03;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
OY 11 ICYTS 15  
DB 4 VCYYT 8

RESULT 9  
S02381  
probable membrane antigen CL1 - human herpesvirus 4 (fragment)  
C:Species: human herpesvirus 4, Epstein-Barr virus  
C:Date: 01-Dec-1989 #sequence\_revision 01-Dec-1989 #text\_change 08-Oct-1999  
C:Accession: S02381  
R:Walls, D.; Gannon, F.  
EMBO J. 7, 1191-1196, 1988  
A:Title: The expression of novel antigens from the Epstein-Barr virus large internal  
A:Reference number: S02381; MUID:88296424; PMID:2841116  
A:Accession: S02381  
A:Molecule type: DNA  
A:Residues: 1-15 <MAL>  
A:Cross-references: EMBL:X07814; NID:959167; PIRN:CMA30673.1; PID:9930013  
C:Keywords: membrane protein; surface antigen

Query Match 28.1% Score 25; DB 2; Length 15;  
Best Local Similarity 66.7%; Pred. No. 1.5e+03;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 4 WCKGR 9  
DB 6 WCKSGR 11

RESULT 10  
S03530  
Ig heavy chain J region (JH-4) - African clawed frog  
C:Species: Xenopus laevis (African clawed frog)  
C:Date: 21-Nov-1993 #sequence\_revision 08-Nov-1996 #text\_change 21-Jul-2000  
C:Accession: S03530  
R:Schwager, J.; Grosberger, D.; du Pasquier, L.  
EMBO J. 7, 2409-2415, 1988  
A:Title: Organization and rearrangement of immunoglobulin M genes in the amphibian Xe  
A:Reference number: S01158; MUID:89052653; PMID:2903824  
A:Accession: S03530  
A:Molecule type: DNA  
A:Residues: 1-14 <SCH>  
A:Cross-references: EMBL:X14918; NID:964805; PIRN:CMA33043.1; PID:91334657

Query Match 27.5% Score 24.5; DB 2; Length 14;  
Best Local Similarity 41.7%; Pred. No. 1.7e+03;  
Matches 5; Conservative 3; Mismatches 3; Indels 1; Gaps 1;  
OY 4 WCKGRICTYS 15  
DB 4 WG-QGTLVTVTS 14

RESULT 11  
A59173  
nuclease Bhl (EC 3.1.-.-) - Basidiobolus haptosporius (fragment)  
C:Species: Basidiobolus haptosporius  
C:Date: 18-Feb-2000 #sequence\_revision 18-Feb-2000 #text\_change 18-Feb-2000  
C:Accession: A59173  
R:Desai, N.; Shankar, V.  
submitted to the Protein Sequence Database, February 2000  
A:Description: Single-strand-specific, guanylic acid preferential nuclease from Basidi  
A:Reference number: A59173  
A:Accession: A59173  
A:Status: preliminary

A:Molecule type: protein  
 A:Residues: 1-10 <DES>  
 A:Cross-references: single-strand-specific nuclease  
 A:Note: extracellular, single-strand-specific nuclease  
 C:Keywords: hydrolase

Query Match 27.0%; Score 24; DB 2; Length 10;  
 Best Local Similarity 37.5%; Pred. No. 1.5e+03;  
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 4 WGCKGRIT 11  
 ||| : :  
 DB 1 WGLIHL 8

## RESULT 12

PH1318 Ig heavy chain DJ region (clone C527-121) - human (fragment)

C:Species: Homo sapiens (man)  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999

C:Accession: PH1318  
 R:Masserman, R.; Gallil, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.

J. Exp. Med. 176, 1577-1581, 1992

A:Title: Predominance of fetal type DJH joining in young children with B precursor lymph

A:Reference number: PH1302; MUID:93094761; PMID:1460419

A:Accession: PH1318

A:Molecule type: DNA

A:Residues: 1-15 <NMS>

C:Keywords: heterotetramer; immunoglobulin

Query Match 27.0%; Score 24; DB 2; Length 15;  
 Best Local Similarity 75.0%; Pred. No. 2.1e+03;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 11 ICYT 14  
 :|||  
 DB 2 VCYT 5

## RESULT 13

PX0062 beta-galactoside-binding lectin - Caenorhabditis elegans (fragment)

C:Species: Caenorhabditis elegans  
 C:Date: 17-Aug-1992 #sequence\_revision 17-Aug-1992 #text\_change 26-May-2000

C:Accession: PX0062  
 R:Hirabayashi, J.; Satoh, M.; Ohyama, Y.; Kasai, K.

J. Biochem. 111, 553-555, 1992

A:Title: Purification and characterization of beta-galactoside-binding proteins from Ca

A:Reference number: PX0062; MUID:92348337; PMID:1639749

A:Accession: PX0062

A:Molecule type: protein

A:Residues: 1-19 <HIR>

C:Superfamily: lactose-binding lectin L-36

Query Match 27.0%; Score 24; DB 2; Length 19;  
 Best Local Similarity 50.0%; Pred. No. 2.5e+03;  
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 NSWGCKGR 9  
 ||| : :  
 DB 10 NEMGNER 17

## RESULT 14

S03532 Ig heavy chain J region (JH-7) - African clawed frog

C:Species: Xenopus laevis (African clawed frog)  
 C:Date: 21-Nov-1993 #sequence\_revision 08-Nov-1996 #text\_change 20-Jun-2000

C:Accession: S03532

R:Schwager, J.; Grossberger, D.; du Pasquier, L.

EMBO J. 7, 2409-2415, 1988

A:Title: Organization and rearrangement of immunoglobulin M genes in the amphibian Xenop

A:Reference number: S01158; MUID:89052653; PMID:2903824

A:Molecule type: DNA  
 A:Residues: 1-16 <SCH>  
 A:Cross-references: EMBL:X14918; NID:G64805; PIDN:CA33046.1; PID:G1334660  
 A:Note: the authors translated the codon AAC for residue 1 as Asp  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 26.4%; Score 23.5; DB 2; Length 16;  
 Best Local Similarity 41.7%; Pred. No. 2.6e+03;  
 Matches 5; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

OY 4 WGCKGRITCYTS 15  
 ||| : : :  
 DB 6 WGTWTVTS 16

## RESULT 15

D49021 Ig heavy chain J7 region - African clawed frog

C:Species: Xenopus laevis (African clawed frog)  
 C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 17-Mar-1999

C:Accession: D49021  
 R:Haite, R.N.; Amemiya, C.T.; Suzuki, D.; Litman, G.W.

J. Exp. Med. 171, 1721-1737, 1990

A:Title: Eleven distinct V-H gene families and additional patterns of sequence variat

A:Reference number: A47624; MUID:90237760; PMID:2110243

A:Accession: D49021

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-16 <HAIT>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 26.4%; Score 23.5; DB 2; Length 16;  
 Best Local Similarity 41.7%; Pred. No. 2.6e+03;  
 Matches 5; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

OY 4 WGCKGRITCYTS 15  
 ||| : : :  
 DB 6 WGTWTVTS 16

## RESULT 16

S57274 triacylglycerol lipase (EC 3.1.1.3) - Psychrobacter immobilis (fragment)

C:Species: Psychrobacter immobilis  
 C:Date: 28-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 03-Nov-1995

C:Accession: S57274  
 R:Arpigny, J.L.; Feller, G.; Gerday, C.

Biochim. Biophys. Acta 1283, 103, 1995

A:Title: Corrigendum to "Cloning, sequence and structural features of a lipase from t

A:Reference number: S57274; MUID:95359197; PMID:7632728

A:Accession: S57274

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-7 <ARP>

A:Cross-references: EMBL:X67712

C:Keywords: carboxylic ester hydrolase

Query Match 25.8%; Score 23; DB 2; Length 7;  
 Best Local Similarity 57.1%; Pred. No. 2.8e+05;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 4 WGCKGRIT 10  
 ||| : :  
 DB 1 WGDKDI 7

## RESULT 17

PH143 Ig heavy chain DJ region (clone C100-91) - human (fragment)

C:Species: Homo sapiens (man)  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999

C:Accession: PH143

R:Wasserman, R.; Galli, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rivera, G.  
J. Exp. Med. 176, 1577-1581, 1992  
A:Title: Predominance of fetal type DHJ joining in young children with B precursor lymph  
A:Reference number: PH1302; MUID:93094761; PMID:1460419  
A:Accession: PH1343  
A:Molecule type: DNA  
A:Residues: 1-11 <MAS>  
C:Keywords: heterotetramer; immunoglobulin

Query Match 25.8%; Score 23; DB 2; Length 11;  
Best Local Similarity 60.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNSMG 5  
DB 4 LDNMG 8

RESULT 18  
146922  
gene Bc1a protein - bovine (fragment)  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 05-Nov-1999  
C:Accession: 146922  
R:Ellis, S.A.; Braem, K.A.; Morrison, W.I.  
Immunogenetics 37, 49-56, 1992  
A:Title: Transmembrane and cytoplasmic domain sequences demonstrate at least two express  
A:Reference number: 146921; MUID:93052564; PMID:1428011  
A:Accession: 146922  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-12 <EL>  
A:Cross-references: GB:547738; MID:9258999; PIDN:AMB23972.1; PID:9259000  
C:Genetics:  
A:Gene: Bc1a

Query Match 25.8%; Score 23; DB 2; Length 12;  
Best Local Similarity 70.0%; Pred. No. 2.5e+03;  
Matches 7; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

OY 5 GCKGRICYT 14  
DB 1 GCKGRIT--YT 8

RESULT 19  
19 H chain V-D-J region (clone B-1ess 230) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999  
C:Accession: PH1639  
R:Levinson, D.A.; Campos-Torres, J.; Leder, P.  
J. Exp. Med. 178, 317-329, 1993  
A:Title: Molecular characterization of transgene-induced immunodeficiency in B-1ess mice  
A:Reference number: PH1580; MUID:93301609; PMID:8315387  
A:Accession: PH1639  
A:Molecule type: DNA  
A:Residues: 1-14 <LEV>  
A:Experimental source: bone marrow pre-B lymphocyte  
C:Keywords: immunoglobulin

Query Match 25.8%; Score 23; DB 2; Length 14;  
Best Local Similarity 50.0%; Pred. No. 2.8e+03;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 8 GRITCY 13  
DB 7 GVLVCY 12

RESULT 20  
A56786  
p1meoy1-coa synthase - Bacillus sphaericus (fragment)

C:Species: Bacillus sphaericus  
C:Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 18-Aug-1995  
C:Accession: A56786  
R:Ploix, O.; Souliard, P.; Marguet, A.; Gloeckler, R.; Lemoine, Y.  
Biochem. J. 287, 685-690, 1992  
A:Title: Investigation of the first step of biotin biosynthesis in Bacillus sphaericus  
A:Reference number: A56786; MUID:93075017; PMID:1445232  
A:Accession: A56786  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-15 <PILO>  
A:Experimental source: Bacillus sphaericus protein overexpressed in Escherichia coli  
A:Note: sequence extracted from NCBI backbone (NCBIP:117639)  
C:Genetics:  
A:Gene: biow  
C:Keywords: biotin biosynthesis; homodimer

Query Match 25.8%; Score 23; DB 2; Length 15;  
Best Local Similarity 60.0%; Pred. No. 3e+03;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 10 IICYT 14  
DB 2 LICYS 6

RESULT 21  
A45103  
7 alpha-hydroxy-4-cholesten-3-one 12 alpha-hydroxylase, cytochrome P450 12a1pha, HCO  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 30-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change 03-Mar-1995  
C:Accession: A45103  
R:Ishida, H.; Noshitro, M.; Okuda, K.; Coon, M.J.  
J. Biol. Chem. 267, 21319-21323, 1992  
A:Title: Purification and characterization of 7 alpha-hydroxy-4-cholesten-3-one 12 al  
A:Reference number: A45103; MUID:93016066; PMID:1400444  
A:Accession: A45103  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-15 <ISH>  
A:Experimental source: liver microsomes  
A:Note: sequence extracted from NCBI backbone (NCBIP:116791)

Query Match 25.8%; Score 23; DB 2; Length 15;  
Best Local Similarity 37.5%; Pred. No. 3e+03;  
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 4 MCCKGRIT 11  
DB 3 MGLLGALL 10

RESULT 22  
A59046  
alpha-conotoxin MII - cone shell (Conus magus)  
C:Species: Conus magus (magus cone)  
C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999  
C:Accession: A59046  
R:Cartier, G.E.; Yoshikami, D.; Gray, W.R.; Luo, S.; Olivera, B.M.; McIntosh, J.M.  
J. Biol. Chem. 271, 7522-7528, 1996  
A:Title: A new alpha-conotoxin which targets alpha3beta2 nicotinic acetylcholine rec  
A:Reference number: A59046; MUID:96205934; PMID:8631783  
A:Accession: A59046  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-16 <CAR>  
C:Superfamily: alpha-conotoxin  
C:Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neu  
F:1-16/Product: alpha-conotoxin MII #status experimental <MAR>  
F:2-8,3-16/Disulfide bonds: #status experimental  
F:16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 25.8%; Score 23; DB 2; Length 16;

Best Local Similarity 33.3%; Pred. No. 3.1e+03;  
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 5 GCKGRICX 13  
||  
1 GCSSNPVCH 9

## RESULT 23

S43958  
Ig mu chain V region (clone 2) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 20-Oct-1994 #sequence\_revision 26-Jul-1996 #text\_change 17-Mar-1999  
C:Accession: S43958  
R:Wagner, S.D.; Williams, G.T.; Larson, T.; Neuberger, M.S.; Kitamura, D.; Rajewsky, K.; Nucleic Acids Res. 22, 1389-1393, 1994  
A:Title: Antibodies generated from human immunoglobulin miniloci in transgenic mice.  
A:Reference number: S43956; MUID:94248036; PMID:8190629  
A:Accession: S43958  
A:Molecule type: DNA  
A:Residues: 1-18 <WAG>  
C:Keywords: immunoglobulin

Query Match 25.8%; Score 23; DB 2; Length 18;  
Best Local Similarity 60.0%; Pred. No. 3.5e+03;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNSWG 5  
::|||  
Db 12 VDSWG 16

## RESULT 24

C39305  
neurotoxin Tx3 - spider (Phoneutria nigriventer) (fragment)  
C:Species: Phoneutria nigriventer  
C:Date: 14-Feb-1992 #sequence\_revision 14-Feb-1992 #text\_change 07-Feb-1997  
C:Accession: C39305  
R:Rezende Jr., L.; Cordeiro, M.N.; Oliveira, E.B.; Diniz, C.R.  
Toxicon 29, 1225-1233, 1991  
A:Title: Isolation of neurotoxic peptides from the venom of the 'armed' spider Phoneutria  
A:Reference number: A39305; MUID:92196803; PMID:1801316  
A:Accession: C39305  
A:Status: Preliminary  
A:Molecule type: protein  
A:Residues: 1-19 <REZ>  
C:Keywords: neurotoxin

Query Match 25.8%; Score 23; DB 2; Length 19;  
Best Local Similarity 80.0%; Pred. No. 3.6e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 GCKGR 9  
||  
Db 1 GCIGR 5

## RESULT 25

S03531  
Ig heavy chain J5 region - African clawed frog  
C:Species: Xenopus laevis (African clawed frog)  
C:Date: 21-Nov-1993 #sequence\_revision 08-Nov-1996 #text\_change 20-Jun-2000  
C:Accession: S03531; C49021  
R:Schwager, J.; Grossberger, D.; du Pasquier, L.  
EMBO J. 7, 2409-2415, 1988  
A:Title: Organization and rearrangement of immunoglobulin M genes in the amphibian Xenopus  
A:Reference number: S01158; MUID:89052653; PMID:2903824  
A:Accession: S03531  
A:Molecule type: DNA  
A:Residues: 1-17 <SCH>  
A:CROSS-References: EMBL:X14918; NID:964805; PIDN:CAA33044.1; PID:q134658  
R:Haite, R.N.; Amemiya, C.T.; Suzuki, D.; Litman, G.W.  
J. Exp. Med. 171, 1721-1737, 1990

A:Title: Eleven distinct V-H gene families and additional patterns of sequence variation  
A:Reference number: A47624; MUID:90237760; PMID:2110243

A:Accession: C49021  
A:Status: Preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 3-17 <HA1>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin

Query Match 25.3%; Score 22.5; DB 2; Length 17;  
Best Local Similarity 41.7%; Pred. No. 3.9e+03;  
Matches 5; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

OY 4 WCKGRICVTS 15  
||  
Db 7 WCA-GTMYTVTS 17

## RESULT 26

A61068  
locustakinin - migratory locust  
C:Species: Locusta migratoria (migratory locust)  
C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 08-Dec-1995  
C:Accession: A61068  
R:Schoofs, L.; Holman, G.M.; Proost, P.; Van Damme, J.; Hayes, T.K.; De Loof, A.  
Regul. Pept. 37, 49-57, 1992  
A:Title: Locustakinin, a novel myotropic peptide from Locusta migratoria, isolation,  
A:Reference number: A61068; MUID:92262851; PMID:1585017  
A:Accession: A61068  
A:Molecule type: protein  
A:Residues: 1-6 <SCH>  
C:Keywords: amidated carboxyl end; cephalomyotropic peptide; neuropeptide  
F:6/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 24.7%; Score 22; DB 2; Length 6;  
Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 NSWG 5  
|||  
Db 3 SSWG 6

## RESULT 27

JS0315  
leucokinin V - Madeira cockroach  
C:Species: Leucophaea maderae (Madeira cockroach)  
C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 20-Jun-2000  
C:Accession: JS0315  
R:Holman, G.M.; Cook, B.J.; Nachman, R.J.  
Comp. Biochem. Physiol. C 88, 27-30, 1987  
A:Title: Isolation, primary structure, and synthesis of leucokinin V and VI: myotrop  
A:Reference number: JS0315  
A:Accession: JS0315  
A:Molecule type: protein  
A:Residues: 1-8 <HOL>  
C:Comment: Leucokinin, a family of cephalomyotropic peptides, stimulate contractile  
C:Keywords: amidated carboxyl end; cephalomyotropic peptide  
F:8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 24.7%; Score 22; DB 2; Length 8;  
Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 NSWG 5  
|||  
Db 5 SSWG 8

## RESULT 28

JS0316  
leucokinin VI - Madeira cockroach  
C:Species: Leucophaea maderae (Madeira cockroach)



C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 20-Jun-2000  
 C:Accession: JS0316  
 R:Holman, G.M.; Cook, B.J.; Nachman, R.J.  
 Comp. Biochem. Physiol. C 88, 27-30, 1987  
 A:Title: Isolation, primary structure, and synthesis of leucokinin V and VI: myotropic  
 A:Reference number: JS0315  
 A:Accession: JS0316  
 A:Molecule type: protein  
 A:Residues: 1-8 <HOL>  
 C:Comment: Leucokinin, a family of cephalomyotropic peptides, stimulate contractile act  
 C:Keywords: amidated carboxyl end; cephalomyotropic peptide; pyroglutamic acid  
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F:8/Modified site: amidated carboxyl end (Gly) #status experimental

Db :|||  
 6 SSWG 9

Search completed: June 5, 2003, 09:00:02  
 Job time : 18 secs

Query Match 24.7% Score 22; DB 2; Length 8;  
 Best Local Similarity 75.0% Pred. No. 2.8e+05;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 NSWG 5  
 :|||  
 Db 5 HSWG 8

RESULT 29  
 JS0317  
 leucokinin VII - Madeira cockroach  
 C:Species: Leucophaea maderae (Madeira cockroach)  
 C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 20-Jun-2000  
 C:Accession: JS0317  
 R:Holman, G.M.; Cook, B.J.; Nachman, R.J.  
 Comp. Biochem. Physiol. C 88, 31-34, 1987  
 A:Title: Isolation, primary structure and synthesis of leucokinin VII and VIII: the fln  
 A:Reference number: JS0317  
 A:Accession: JS0317  
 A:Molecule type: protein  
 A:Residues: 1-8 <HOL>  
 C:Comment: Leucokinin, a family of cephalomyotropic peptides, stimulate contractile act  
 C:Keywords: amidated carboxyl end; cephalomyotropic peptide  
 F:8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 24.7% Score 22; DB 2; Length 8;  
 Best Local Similarity 75.0% Pred. No. 2.8e+05;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 NSWG 5  
 :|||  
 Db 5 SSWG 8

RESULT 30  
 A24244  
 adipokinetin hormone - bollworm  
 N:Alternate names: Hez-AKH  
 C:Species: Heliothis zea (bollworm, corn earworm, tomato fruitworm)  
 C:Date: 31-Mar-1988 #sequence\_revision 23-Mar-1995 #text\_change 31-Oct-1997  
 C:Accession: A24244  
 R:Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Holman, G.M.; Wagner, R.M.; Ridgway  
 Biochem. Biophys. Res. Commun. 135, 622-628, 1986  
 A:Title: Isolation and primary structure of a peptide from the corpora cardiaca of Helic  
 A:Reference number: A24244; MUID:86186794; PMID:3964263  
 A:Accession: A24244  
 A:Molecule type: protein  
 A:Residues: 1-9 <JAF>  
 C:Superfamily: adipokinetin hormone  
 C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic  
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F:9/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 24.7% Score 22; DB 2; Length 9;  
 Best Local Similarity 75.0% Pred. No. 2.8e+05;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 NSWG 5

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 5, 2003, 08:58:43 ; Search time 11 Seconds

(without alignments)

56.559 Million cell updates/sec

Title: US-09-605-573a-69\_COPY\_12-26

Perfect score: 89

Sequence: 1 LNSWCKGRITCYNS 15

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 1147

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	30.3	8	1	LCK1_LEUMA
2	27	30.3	8	1	LCK3_LEUMA
3	27	30.3	20	1	LEC1_ARTIN
4	26	29.2	19	1	DURC_STRGP
5	26	29.2	19	1	LANC_STRSO
6	25.5	28.7	19	1	LANA_ACTLG
7	23	25.8	12	1	CX13_CONNR
8	23	25.8	16	1	CX12_CONNR
9	23	25.8	19	1	TX3_PHONI
10	22	24.7	6	1	LCK1_LOCM1
11	22	24.7	8	1	LCK2_LEUMA
12	22	24.7	8	1	LCK4_LEUMA
13	22	24.7	8	1	LCK5_LEUMA
14	22	24.7	8	1	LCK6_LEUMA
15	22	24.7	8	1	LCK7_LEUMA
16	22	24.7	11	1	CEP1_ACHFU
17	22	24.7	15	1	LCK_DROME
18	22	24.7	19	1	GOME_ACAGO
19	22	24.7	19	1	SCX6_TITBA
20	22	24.7	20	1	LEC3_ARTIN
21	21	23.6	8	1	LCK8_LEUMA
22	21	23.6	17	1	TAC1_TACGI
23	21	23.6	17	1	TAC3_TACGI
24	20	22.5	11	1	CX11_CONNR
25	20	22.5	12	1	TYN3_HOPTI
26	20	22.5	13	1	CX14_CONNR
27	20	22.5	14	1	SMS1_MYOSC
28	20	22.5	14	1	SMS_ALIMI
29	20	22.5	15	1	CX1B_CONNR
30	19	21.3	9	1	ISOT_CYPCA
31	19	21.3	9	1	OXYT_RATCL
32	19	21.3	11	1	TYN4_HOPTI
33	19	21.3	12	1	CX11_CONNR

34	19	21.3	14	1	SAP2_ARBP
35	19	21.3	14	1	SCR3_LEQU
36	19	21.3	17	1	ROBR_CHITE
37	19	21.3	17	1	TPIS_PINPS
38	19	21.3	18	1	PPM1_LIMPO
39	19	21.3	18	1	PPM2_LIMPO
40	19	21.3	19	1	CXR_CONTU
41	19	21.3	20	1	CUDE_VERCH
42	19	21.3	20	1	THIO_CANFA
43	18	20.2	10	1	HTE1_ROMNI
44	18	20.2	10	1	HTE2_CARMO
45	18	20.2	10	1	HTE_HELZE
46	18	20.2	13	1	TEML_RANTE
47	18	20.2	14	1	CALI_CALGI
48	18	20.2	15	1	TAL_TREPR
49	18	20.2	15	1	UC19_MAIZE
50	18	20.2	17	1	CXMA_CONPE
51	18	20.2	17	1	CXMA_CONPE
52	17.5	19.7	18	1	HSTB_ECOLI
53	17	19.1	8	1	ACT_THUAL
54	17	19.1	10	1	BPP8_BOTIN
55	17	19.1	10	1	HTE_NAUCI
56	17	19.1	10	1	HTE_TABAT
57	17	19.1	10	1	LABA_JATMU
58	17	19.1	13	1	MIA_AMOCA
59	17	19.1	13	1	MIA_CAMDR
60	17	19.1	14	1	NO40_VICSA
61	17	19.1	14	1	MAST_VESBA
62	17	19.1	15	1	CX13_CONNR
63	17	19.1	15	1	CX12_CONNR
64	17	19.1	15	1	RMGG_CARCR
65	17	19.1	15	1	UC08_MAIZE
66	17	19.1	16	1	CX11_CONNR
67	17	19.1	16	1	CX13_CONNR
68	17	19.1	17	1	FLAW_AZOCH
69	17	19.1	17	1	RANR_RANRU
70	17	19.1	18	1	MLB_HORSE
71	17	19.1	18	1	MLB_SCYCA
72	17	19.1	20	1	FLAW_AZOVI
73	17	19.1	20	1	HG11_FASHE
74	17	19.1	20	1	LEC2_MACPO
75	17	19.1	20	1	LEC3_MACPO
76	17	19.1	20	1	OMPI_ACRAC
77	16	18.0	9	1	OXYA_SCYCA
78	16	18.0	9	1	OXYA_SCYCA
79	16	18.0	9	1	OXYA_SCYCA
80	16	18.0	9	1	OXYT_BURE
81	16	18.0	9	1	OXYT_CYPCA
82	16	18.0	9	1	OXYT_OCTVU
83	16	18.0	9	1	OXYT_RABIT
84	16	18.0	9	1	OXYT_RABIT
85	16	18.0	10	1	GLEW_HUMAN
86	16	18.0	11	1	TYN1_HOPTI
87	16	18.0	12	1	CXST_CONTE
88	16	18.0	12	1	V14K_MSSV
89	16	18.0	13	1	TEMA_RANTE
90	16	18.0	13	1	YRNP_PROLU
91	16	18.0	14	1	LPW_CITFR
92	16	18.0	14	1	LPW_SALTY
93	16	18.0	14	1	UHA2_CANFA
94	16	18.0	14	1	UN37_CLOPA
95	16	18.0	15	1	ALIS_MANSE
96	16	18.0	15	1	KLOM_LUNTE
97	16	18.0	15	1	UC23_MAIZE
98	16	18.0	16	1	FIBA_MUSVI
99	16	18.0	16	1	FIBA_RABIT
100	16	18.0	16	1	PA2_NAUSP

## ALIGNMENTS

RESULT 1

P11760 arbacia pun  
P4561 leturus qui  
P58025 chlorobium  
P8166 pinus pines  
P14215 limulus pol  
P14216 limulus pol  
P58811 conus tulip  
P80406 verticillium  
P99505 canis fam1  
P18110 romalea mic  
P11385 carausius m  
P16535 heliothis z  
P57104 rana tempor  
P20728 calotrophi  
P34070 liemella br  
P80625 zea mays (m  
P58926 conus penna  
P58927 conus penna  
P01560 escherichia  
P18691 thunnus alb  
P30426 bochops in  
P10939 nauphoeta c  
P14596 tabanura atr  
P13270 jatropha mu  
P41589 anolis caro  
P01198 camelus dro  
P55961 vicia sativ  
P21654 vespa basai  
P58842 conus querc  
P56640 conus aulic  
P21586 caretta car  
P6014 zea mays (m  
P56639 conus aulic  
P56641 conus aulic  
P23002 azotobacter  
P08952 rana rugosa  
P01202 equus cabal  
P01206 scyllorhinu  
P52964 azotobacter  
P80527 fasciola he  
P18677 macula pom  
P20242 actinobacil  
P42996 scyllorhinu  
P42997 scyllorhinu  
P42995 bufu regula  
P23879 cyprinus ca  
P80027 octopus vul  
P32878 oryctolagus  
P43000 squallus aca  
P02728 homo sapien  
P82651 hoplobatr  
P58846 conus texti  
P82006 white spot  
P56317 rana tempor  
P41122 photorhabdu  
P03056 citrobacter  
P03054 salmonella  
P99506 canis fam1  
P81358 clostridium  
P43555 manduca sex  
P11918 lumbricus t  
P80629 zea mays (m  
P14458 mustela vis  
P14461 oryctolagus  
Q10756 naja sputat

LCK1\_LEDMA STANDARD: PRT: 8 AA.  
 AC P21140;  
 DT 01-MAY-1991 (Rel. 18, Created)  
 DT 01-MAY-1991 (Rel. 18, Last sequence update)  
 DT 01-MAY-1991 (Rel. 18, Last annotation update)  
 DE Leucokinin I (L-1).  
 OS Leucophaea maderae (Madeira cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
 OC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;  
 OC Blaberoidea; Blaberidae; Leucophaea.  
 OX NCBI\_Taxid=6988;  
 RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RC TISSUE-Head;  
 RA Holman G.M., Cook B.J., Nachman R.J.;  
 RT "Isolation, primary structure and synthesis of two neuropeptides  
 from Leucophaea maderae: members of a new family of  
 Cephalomyotroptins.";  
 RT Cephalomyotroptins.";  
 RL Comp. Biochem. Physiol. 84C:205-211(1986).  
 CC -1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE  
 ACTIVITY OF COCKROACH PROTODERM (HINDGUT).  
 CC -1- SIMILARITY: TO THE OTHER LEUCOKININS.  
 KW Neuropeptide; Amidation.  
 FT MOD.RES 8  
 SQ SEQUENCE 8 AA; 893 MW; DC635B449C64; CRC64;  
 QY Query Match 30.3%; Score 27; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 5 NSWG 8  
 RESULT 2  
 LCK3\_LEDMA STANDARD: PRT: 8 AA.  
 AC P21142;  
 DT 01-MAY-1991 (Rel. 18, Created)  
 DT 01-MAY-1991 (Rel. 18, Last sequence update)  
 DT 01-MAY-1991 (Rel. 18, Last annotation update)  
 DE Leucokinin III (L-III).  
 OS Leucophaea maderae (Madeira cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
 OC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;  
 OC Blaberoidea; Blaberidae; Leucophaea.  
 OX NCBI\_Taxid=6988;  
 RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RC TISSUE-Head;  
 RA Holman G.M., Cook B.J., Nachman R.J.;  
 RT "Primary structure and synthesis of two additional neuropeptides  
 from Leucophaea maderae: members of a new family of  
 Cephalomyotroptins.";  
 RT Cephalomyotroptins.";  
 RL Comp. Biochem. Physiol. 84C:271-276(1986).  
 CC -1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE  
 ACTIVITY OF COCKROACH PROTODERM (HINDGUT).  
 CC -1- SIMILARITY: TO THE OTHER LEUCOKININS.  
 KW Neuropeptide; Amidation.  
 FT MOD.RES 8  
 SQ SEQUENCE 8 AA; 910 MW; DC635B449C64; CRC64;  
 QY Query Match 30.3%; Score 27; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 5 NSWG 8

RESULT 3  
 LECT\_ARTIN STANDARD: PRT: 20 AA.  
 AC P18671;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 01-NOV-1990 (Rel. 35, Last annotation update)  
 DE Agglutinin beta-1 chain (Jacalin beta-1 chain).  
 OS Artocarpus integrifolia (Jack fruit) (Artocarpus integrifolia).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eucosids I; Rosales; Moraceae; Artocarpus.  
 OX NCBI\_Taxid=3490;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE-Seed;  
 RA Young N.M., Johnston R.A.Z., Szabo A.G., Watson D.C.;  
 RT "Homology of the D-galactose-specific lectins from Artocarpus  
 integrifolia and MacLura pomifera and the role of an unusual small  
 polypeptide subunit.";  
 RT Arch. Biochem. Biophys. 270:596-603(1989).  
 RN [2]  
 RP SEQUENCE.  
 RX MEDLINE=92287028; PubMed=1599414;  
 RA Mahanta S.K., Sankar S., Prasad Rao N.V.S.A.V., Swamy M.J.,  
 RA Suroolia A.;  
 RT "Primary structure of a Thomsen-Friedenreich antigen-specific lectin,  
 jacalin [Artocarpus integrifolia (jack fruit) agglutinin]. Evidence  
 for the presence of an internal repeat.";  
 RT Biochem. J. 284:95-101(1992).  
 RN [3]  
 RP SEQUENCE.  
 RX MEDLINE=93152601; PubMed=8427879;  
 RA Ngoc L.D., Brillard M., Hoebeke J.;  
 RT "The alpha- and beta-subunits of the jacalins are cleavage products  
 from a 17-kDa precursor.";  
 RT Biochim. Biophys. Acta 1156:219-222(1993).  
 RN [4]  
 RP X-RAY CRYSTALLOGRAPHY (2.43 ANGSTROMS).  
 RX MEDLINE=9626349; PubMed=8673603;  
 RA Sakaranarayanan R., Sekar S., Banerjee R., Sharma V., Suroolia A.,  
 RA Vijayan M.;  
 RT "A novel mode of carbohydrate recognition in jacalin, a Moraceae  
 plant lectin with a beta-prism fold.";  
 RL Nat. Struct. Biol. 3:596-603(1996).  
 CC -1- FUNCTION: D-GALACTOSE-SPECIFIC LECTIN, BINDS THE T-ANTIGEN  
 STRUCTURE GAL-BETA1-3-GALNAc (THOMSEN-FRIEDENREICH-ANTIGEN-  
 SPECIFIC LECTIN).  
 CC -1- FUNCTION: POTENT AND SELECTIVE STIMULANT OF DISTINCT T- AND B-CELL  
 FUNCTIONS. SHOWS A UNIQUE ABILITY TO SPECIFICALLY RECOGNIZE IGA-1  
 FROM HUMAN SERUM.  
 CC -1- SUBUNIT: Tetramer of four alpha chain associated with two or four  
 beta chains.  
 CC -1- SIMILARITY: TO THE OTHER AGGLUTININ BETA CHAINS.  
 DR PIR: S03983; S03983.  
 DR PIR: S29638; S29638.  
 DR PDB: 1JAC; 05-JUN-97.  
 KW Lectin; IGA-binding protein; 3D-structure.  
 SQ SEQUENCE 20 AA; 2062 MW; 894AFC95F4DDE248 CRC64;  
 QY Query Match 30.3%; Score 27; DB 1; Length 20;  
 Best Local Similarity 57.1%; Pred. No. 2.2e+02;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 DB 12 VGSWGAK 18

RESULT 4  
 DUCR\_STRCP STANDARD: PRT: 19 AA.  
 ID DUCR\_STRCP

AC P36503;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 16-OCT-1994 (Rel. 29, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Lanthibiotic duramycin C.  
 OS Streptomyces griseolentus.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.  
 RX NCBI\_TaxID=29306;  
 RN (1)  
 RP SEQUENCE.  
 RC STRAIN=R2107;  
 RX MEDLINE=91107436; PubMed=2125590;  
 RA Friedenham A., Fendrich G., Markl F., Markl W., Gruner J.,  
 RA Raschdorf F., Peter H.H.;  
 RA "Duramycins B and C, two new lanthionine containing antibiotics as  
 RT inhibitors of phospholipase A2. Structural revision of duramycin and  
 RT cinamycin.";  
 RL J. Antibiot. 43:1403-1412(1990).  
 RN (2)  
 RP STRUCTURE BY NMR.  
 RA Zimmermann N., Freund S., Friedenham A., Jung G.;  
 RT "Solution structure of the lantibiotics duramycin B and C.";  
 RL Eur. J. Biochem. 216:419-428(1993).  
 CC -1- FUNCTION: ACTS AS INHIBITOR OF PHOSPHOLIPASE A2.  
 CC -1- PTM: MATURATION OF LANTIBIOTICS INVOLVES THE ENZYMIC CONVERSION OF  
 CC THR, SER, AND CYS INTO DEHYDRATED AA AND THE FORMATION OF SULFIDE  
 CC BRIDGES. THIS IS FOLLOWED BY THE MEMBRANE TRANSLOCATION AND  
 CC CLEAVAGE OF THE MODIFIED PRECURSOR.  
 CC -1- SIMILARITY: STRUCTURAL SIMILARITY TO OTHER TYPE B LANTIBIOTICS.  
 CC Antibiotic; Bacteriocin; Lantibiotic.  
 FT MOD\_RES 4 4  
 FT MOD\_RES 6 6  
 FT MOD\_RES 11 11  
 FT MOD\_RES 18 18  
 FT MOD\_RES 19 19  
 FT MOD\_RES 19 19  
 FT THIOETH 1 1  
 FT THIOETH 4 4  
 FT THIOETH 5 5  
 FT THIOETH 11 11  
 SQ SEQUENCE 19 AA; 2007 MW; E2404EC3F95286A CRC64;  
 Query Match Score 26; DB 1; Length 19;  
 Best Local Similarity 50.0%; Pred. No. 3.1e+02;  
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 3 SMCCKG 8  
 DB 11 TWSCKG 16  
 RESULT 5  
 LANC\_STRSQ STANDARD; PRT; 19 AA.  
 ID LANC\_STRSQ  
 AC P38655;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Lanthibiotic ancovenin.  
 OS Streptomyces sp. (Strain A647P-2).  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.  
 RX NCBI\_TaxID=1931;  
 RN (1)  
 RP SEQUENCE.  
 RA Makamiya T., Ueki Y., Shiba T., Kido Y., Motoki Y.;  
 RA "The structure of ancovenin, a new peptide inhibitor of angiotensin I

RT converting enzyme.";  
 RL Tetrahedron Lett. 26:665-668(1985).  
 CC -1- FUNCTION: ACTS AS INHIBITOR OF ANGIOTENSIN I CONVERTING ENZYME.  
 CC -1- SIMILARITY: STRUCTURAL SIMILARITY TO OTHER TYPE B LANTIBIOTICS.  
 DR PIR; A61284; EWSMAN.  
 KW Antibiotic; Bacteriocin; Lantibiotic.  
 FT MOD\_RES 4 4  
 FT MOD\_RES 6 6  
 FT MOD\_RES 11 11  
 FT MOD\_RES 18 18  
 FT MOD\_RES 19 19  
 FT MOD\_RES 19 19  
 FT THIOETH 1 1  
 FT THIOETH 4 4  
 FT THIOETH 5 5  
 FT THIOETH 11 11  
 SQ SEQUENCE 19 AA; 2033 MW; F434299E2736286A CRC64;  
 Query Match Score 26; DB 1; Length 19;  
 Best Local Similarity 50.0%; Pred. No. 3.1e+02;  
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 3 SMCCKG 8  
 DB 11 TWSCKG 16  
 RESULT 6  
 LANA\_ACTIG STANDARD; PRT; 19 AA.  
 ID LANA\_ACTIG  
 AC P56650;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Lanthibiotic actagardine (Gardimycin).  
 OS Actinoplanes ligulata.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Micromonosporineae; Micromonosporaceae.  
 RX NCBI\_TaxID=69484;  
 RN (1)  
 RP PRELIMINARY SEQUENCE, AND STRUCTURE BY NMR.  
 RA MEDLINE=91008696; PubMed=2211371;  
 RA Kettentrung J.K., Malabarida A., Vekey K., Cavallieri B.;  
 RT "Sequence determination of actagardine, a novel lantibiotic, by  
 RT homonuclear 2D NMR spectroscopy.";  
 RL J. Antibiot. 43:1082-1088(1990).  
 RN (2)  
 RP SEQUENCE, AND STRUCTURE BY NMR.  
 RA MEDLINE=95255286; PubMed=7737178;  
 RA Zimmermann N., Metzger J.W., Jung G.;  
 RT "The tetracyclic lantibiotic actagardine, 1H-NMR and 13C-NMR  
 RT assignments and revised primary structure.";  
 RL Eur. J. Biochem. 228:786-797(1995).  
 RN (3)  
 RP STRUCTURE BY NMR.  
 RA MEDLINE=97363218; PubMed=9219543;  
 RA Zimmermann N., Jung G.;  
 RT "The three-dimensional solution structure of the lantibiotic aureli-  
 RT biosynthesis-inhibitor actagardine determined by NMR.";  
 RL Eur. J. Biochem. 246:809-819(1997).  
 CC -1- FUNCTION: HAS ANTIBACTERIAL ACTIVITY AGAINST SOME GRAM-POSITIVE  
 CC BACTERIA. HAS GOOD ANTISTREPTOCOCCAL ACTIVITY.  
 DR PDB; 1AL1; 15-OCT-97.  
 KW Antibiotic; Bacteriocin; Lantibiotic; 3D-structure.  
 FT MOD\_RES 1 1  
 FT MOD\_RES 7 7  
 FT MOD\_RES 9 9  
 FT MOD\_RES 14 14  
 FT MOD\_RES 19 19  
 FT MOD\_RES 19 19  
 FT THIOETH 1 1  
 FT THIOETH 7 7  
 FT THIOETH 9 9  
 FT THIOETH 14 14  
 FT THIOETH 19 19  
 SQ SEQUENCE 19 AA; 1962 MW; 5C1391CBEB8765B3 CRC64;

Query Match 28.7%; Score 25.5; DB 1; Length 19;  
 Best Local Similarity 31.2%; Pred. No. 3.7e+02;  
 Matches 5; Conservative 2; Mismatches 4; Indels 5; Gaps 1;

OY 2 NSMGCK----GRITC 12  
 : : : : :  
 DB 2 SGWCTLTRECGTVIC 17

RESULT 7  
 ID CXL3\_CONMR STANDARD: PRT: 12 AA.  
 AC P58809;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Lambda-conotoxin CMrx.  
 OS Conus marmoreus (Marble cone).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
 OC Neogastropoda; Conoidea; Conidae; Conus.  
 OX NCBI\_TaxID=42752;  
 RN [1]  
 RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.  
 RC TISSUE-Venom;  
 RA Balaji R.A., Ohtake A., Sato K., Gopalakrishnakone P., Kini R.M.,  
 Seow K.T., Bay B.-H.;  
 RT "Lambda-conotoxins, a new family of conotoxins with unique disulfide  
 pattern and protein folding. Isolation and characterization from the  
 venom of Conus marmoreus."  
 RL J. Biol. Chem. 275:39516-39522(2000).  
 CC -1- FUNCTION: Inhibits the neuronal noradrenaline transporter.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.  
 CC -1- MASS SPECTROMETRY: MM=1262.77; MW ERR=0.07; METHOD=Electrospray.  
 CC -1- SIMILARITY: BELONGS TO THE CHI/LAMBDA-CONOTOXIN FAMILY.  
 KM Neurotoxin; Toxin; Hydroxylation.  
 FT DISULFID 3 12  
 FT MOD.RES 4 9  
 FT 11 11 HYDROXYLATION.  
 FT MOD.RES 11 11  
 SQ SEQUENCE 12 AA; 1251 MW; 277AAE2422D5A2C8 CRC64;

Query Match 25.8%; Score 23; DB 1; Length 12;  
 Best Local Similarity 50.0%; Pred. No. 6.2e+02;  
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 6 CKGRITCY 13  
 : : : : :  
 DB 3 CCGVSFCY 10

RESULT 8  
 ID CXL2\_CONMA STANDARD: PRT: 16 AA.  
 AC P56636;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Alpha-conotoxin MII (M2).  
 OS Conus magus (Magus cone).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
 OC Neogastropoda; Conoidea; Conidae; Conus.  
 OX NCBI\_TaxID=6492;  
 RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RC TISSUE-Venom;  
 RA MEDLINE=96205934; PubMed=8631783;  
 RA Carrier G.E., Yoshikami D., Gray W.R., Luo S., Olivera B.M.,  
 McIntosh J.M.;  
 RT "A new alpha-conotoxin which targets alpha3beta2 nicotinic  
 acetylcholine receptors."  
 RL J. Biol. Chem. 271:7522-7528(1996).

RN [2]  
 RP STRUCTURE BY NMR.  
 RX MEDLINE=98062282; PubMed=9398298;  
 RA Shon K.-J., Koerber S.C., Rivier J.E., Olivera B.M., McIntosh J.M.;  
 RT "Three-dimensional solution structure of alpha-conotoxin MII, an  
 alpha3beta2 neuronal nicotinic acetylcholine receptor-targeted  
 ligand."  
 RT Biochemistry 36:15693-15700(1997).  
 RL [3]  
 RP STRUCTURE BY NMR.  
 RX MEDLINE=99060038; PubMed=9843366;  
 RA Hill J.M., Oomen C.J., Miranda L.P., Bingham J.-P., Alewood P.F.,  
 Craik D.J.;  
 RT "Three-dimensional solution structure of alpha-conotoxin MII by NMR  
 spectroscopy: effects of solution environment on helicity."  
 RL Biochemistry 37:15621-15630(1998).  
 CC -1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY  
 BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS  
 INHIBIT THEM. THIS PEPTIDE BLOCKS MAMMALIAN NICOTINIC  
 ACETYLCHOLINE RECEPTORS COMPOSED OF ALPHA-3/BETA-2 SUBUNITS. IT  
 HAS AN ACTIVITY 2 TO 4 ORDERS OF MAGNITUDE LESS POTENT ON OTHER  
 NACHR SUBUNIT COMBINATIONS.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.  
 CC -1- SIMILARITY: BELONGS TO THE A SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE  
 FAMILY.  
 DR PDB: 1MI1; 21-OCT-98.  
 DR PDB: 1M2C; 13-JAN-99.  
 KM Postsynaptic neurotoxin; Neurotoxin; Toxin;  
 KM Acetylcholine receptor inhibitor; Antidation; 3D-structure.  
 FT DISULFID 2 8  
 FT DISULFID 3 16  
 FT MOD.RES 16 16 AMIDATION.  
 FT MOD.RES 16 16  
 SQ SEQUENCE 16 AA; 1716 MW; 282AEF190166CAF9 CRC64;

Query Match 25.8%; Score 23; DB 1; Length 16;  
 Best Local Similarity 33.3%; Pred. No. 8.1e+02;  
 Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 5 GCKGRITCY 13  
 : : : : :  
 DB 1 GCCSNPVCH 9

RESULT 9  
 ID TX3\_PHONI STANDARD: PRT: 19 AA.  
 AC P31010;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Neurotoxin TX3 (Fragment).  
 OS Phosphotriphosphatase (Brazilian armed spider).  
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;  
 OC Araneomorphae; Entelegynae; Lycosidae; Ctenidae; Phneutria.  
 OX NCBI\_TaxID=6918;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE-Venom;  
 RX MEDLINE=92196803; PubMed=1801316;  
 RA Rezende L. Jr., Cordeiro M.N., Oliveira E.B., Diniz C.R.;  
 RT "Isolation of neurotoxic peptides from the venom of the 'armed'  
 spider Phosphotriphosphatase (Brazilian armed spider)."  
 RL Toxicon 29:1225-1233(1991).  
 CC -1- FUNCTION: ANTAGONIST OF L-TYPE CALCIUM CHANNELS (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.  
 CC -1- SIMILARITY: BELONGS TO THE SPIDER TOXIN TX3 FAMILY.  
 DR PIR: C39305; C39305.  
 KM Calcium channel inhibitor; Toxin; Neurotoxin.  
 FT NON-TER 19  
 FT 19  
 SQ SEQUENCE 19 AA; 2244 MW; 3214E89CF10F7587 CRC64;

Query Match 25.8%; Score 23; DB 1; Length 19;  
 Best Local Similarity 80.0%; Pred. No. 9.4e+02;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 GCKGR 9  
 : : :  
 DB 1 CIGR 5

RESULT 10  
 LCK1\_LOCKMI STANDARD; PRT; 6 AA.  
 AC P41491;

DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE Locustakinin I.  
 OS Locusta migratoria (Migratory locust).  
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
 CC Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caellifera;  
 CC Acridomorpha; Acridoidea; Acrididae; Oedipodinae; Locusta.  
 OX NCBI\_TaxID=7004;

RA de Loof A.; Holman G.M.; Proost P.; van Damme J.; Hayes T.K.;  
 RA "Locustakinin, a novel myotropic peptide from locusta migratoria,  
 RT isolation, primary structure and synthesis.";  
 RL Regul. Pept. 37:45-57(1992).  
 CC -1- FUNCTION: MYOTROPIC PEPTIDE. MAY BE IMPORTANT IN THE STIMULATION  
 OF ION TRANSPORT AND INHIBITION OF DIURETIC ACTIVITY IN MALPIGHIAN  
 TUBULES.  
 DR PIR: A61068; A61068.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 6  
 SQ SEQUENCE 6 AA; 654 MW; 686365A5B9CDB000 CRC64;

Query Match 24.7%; Score 22; DB 1; Length 6;  
 Best Local Similarity 75.0%; Pred. No. 1.1e+05;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 NSWG 5  
 : : :  
 DB 3 SSWG 6

RESULT 11  
 LCK2\_LEUMA STANDARD; PRT; 8 AA.  
 ID LCK2\_LEUMA  
 AC P21141;

DT 01-MAY-1991 (Rel. 18, Created)  
 DT 01-MAY-1991 (Rel. 18, Last sequence update)  
 DT 01-MAY-1991 (Rel. 18, Last annotation update)  
 DE Leucokinin II (L-II).  
 OS Leucophaea maderae (Madeira cockroach).  
 CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
 CC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;  
 CC Blaberoidea; Blaberidae; Leucophaea.  
 OX NCBI\_TaxID=6988;  
 OX NCBI\_TaxID=6988;  
 RP SEQUENCE, AND SYNTHESIS.  
 RC TISSUE-Head;  
 RA Holman G.M.; Cook B.J.; Nachman R.J.;

RT "Isolation, primary structure and synthesis of two neuropeptides  
 from Leucophaea maderae: members of a new family of  
 Cephalomyotropeptides.";  
 RL Comp. Biochem. Physiol. 84C:205-211(1986).  
 CC -1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE  
 ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).  
 CC -1- SIMILARITY: TO THE OTHER LEUCOKININS.  
 KW Neuropeptide; Amidation.

FT MOD\_RES 8  
 SQ SEQUENCE 8 AA; 852 MW; DC6365A5B9CDB076A CRC64;

Query Match 24.7%; Score 22; DB 1; Length 8;  
 Best Local Similarity 75.0%; Pred. No. 1.1e+05;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 NSWG 5  
 : : :  
 DB 5 SSWG 8

RESULT 12  
 LCK4\_LEUMA STANDARD; PRT; 8 AA.  
 ID LCK4\_LEUMA  
 AC P21143;

DT 01-MAY-1991 (Rel. 18, Created)  
 DT 01-MAY-1991 (Rel. 18, Last sequence update)  
 DT 01-MAY-1991 (Rel. 18, Last annotation update)  
 DE Leucokinin IV (L-IV).  
 OS Leucophaea maderae (Madeira cockroach).  
 CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
 CC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;  
 CC Blaberoidea; Blaberidae; Leucophaea.  
 OX NCBI\_TaxID=6988;  
 OX NCBI\_TaxID=6988;  
 RP SEQUENCE, AND SYNTHESIS.  
 RC TISSUE-Head;  
 RA Holman G.M.; Cook B.J.; Nachman R.J.;

RT "Primary structure and synthesis of two additional neuropeptides  
 from Leucophaea maderae: members of a new family of  
 Cephalomyotropeptides.";  
 RL Comp. Biochem. Physiol. 84C:271-276(1986).  
 CC -1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE  
 ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).  
 CC -1- SIMILARITY: TO THE OTHER LEUCOKININS.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 8  
 SQ SEQUENCE 8 AA; 906 MW; DC6365B1E9D5BDDA CRC64;

Query Match 24.7%; Score 22; DB 1; Length 8;  
 Best Local Similarity 75.0%; Pred. No. 1.1e+05;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 NSWG 5  
 : : :  
 DB 5 SSWG 8

RESULT 13  
 LCK5\_LEUMA STANDARD; PRT; 8 AA.  
 ID LCK5\_LEUMA  
 AC P19987;

DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Leucokinin V (L-V).  
 OS Leucophaea maderae (Madeira cockroach).  
 CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
 CC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;  
 CC Blaberoidea; Blaberidae; Leucophaea.  
 OX NCBI\_TaxID=6988;  
 OX NCBI\_TaxID=6988;  
 RP SEQUENCE, AND SYNTHESIS.  
 RC TISSUE-Head;  
 RA Holman G.M.; Cook B.J.; Nachman R.J.;

RT "Isolation, primary structure, and synthesis of leucokinin V and VI:  
 myotropic peptides of Leucophaea maderae.";  
 RL Comp. Biochem. Physiol. 88C:27-30(1987).  
 CC -1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE  
 ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).  
 CC -1- SIMILARITY: TO THE OTHER LEUCOKININS.

DR PIR: JS0315; JS0315.  
 KW Neuropeptide; Amidation.  
 FT MOD.RES 8  
 SQ SEQUENCE 8 AA; 784 MW; 736365A5B9C865B8 CRC64;

Query Match 24.7%; Score 22; DB 1; Length 8;  
 Best Local Similarity 75.0%; Pred. No. 1.1e+05;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 NSWG 5  
 : : :  
 : : :  
 Db 5 SSWG 8

RESULT 14  
 LCK6\_LEUMA STANDARD; PRT; 8 AA.

AC P19988;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Leucokinin VI (L-VI).  
 OS Leucophaea maderae (Madeira cockroach).  
 CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
 CC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;  
 CC Blaberidae; Blaberidae; Leucophaea.  
 OC NCBI\_TaxID=6986;  
 RN [1]  
 RP SEQUENCE.

RC TISSUE-Head; MEDLINE=87052651; PubMed=2877794;  
 RX Holman G.M., Cook B.J., Nachman R.J.;  
 RT "Isolation, primary structure, and synthesis of leucokinin V and VI:  
 RT myotropic peptides of leucophaea maderae.";  
 RL Comp. Biochem. Physiol. 88C:27-30(1987).  
 CC -1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE  
 CC ACTIVITY OF COCKROACH PROTOPODEM (HINDGUT).  
 CC -1- SIMILARITY: TO THE OTHER LEUCOKININS, AND TO MANDUCA SEXTA AND  
 CC HELIOTHRIS ZEA ADIPOKINETIC HORMONE.  
 DR PIR: JS0316; JS0316.  
 KM Neuropeptide; Amidation.  
 FT MOD.RES 1 8  
 FT MOD.RES 8 AA; 935 MW; 906365B1E9D5A5A6 CRC64;  
 SQ SEQUENCE

Query Match 24.7%; Score 22; DB 1; Length 8;  
 Best Local Similarity 75.0%; Pred. No. 1.1e+05;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 NSWG 5  
 : : :  
 : : :  
 Db 5 SSWG 8

RESULT 15  
 LCK7\_LEUMA STANDARD; PRT; 8 AA.

AC P19989;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 01-FEB-1991 (Rel. 17, Last annotation update)  
 DE Leucokinin VII (L-VII).  
 OS Leucophaea maderae (Madeira cockroach).  
 CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
 CC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;  
 CC Blaberidae; Blaberidae; Leucophaea.  
 OC NCBI\_TaxID=6988;  
 RN [1]  
 RP SEQUENCE.

RC TISSUE-Head; Cook B.J., Nachman R.J.;  
 RA Holman G.M., "Isolation, primary structure and synthesis of leucokinin VII and  
 RT VIII: the final members of this new family of cephalomyotropic

RT peptides isolated from head extracts of leucophaea maderae.";  
 RL Comp. Biochem. Physiol. 88C:31-34(1987).  
 CC -1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE  
 CC ACTIVITY OF COCKROACH PROTOPODEM (HINDGUT).  
 CC -1- SIMILARITY: TO THE OTHER LEUCOKININS.  
 DR PIR: JS0317; JS0317.  
 KW Neuropeptide; Amidation.  
 FT MOD.RES 8  
 SQ SEQUENCE 8 AA; 866 MW; D6365A5B9C9C76A CRC64;

Query Match 24.7%; Score 22; DB 1; Length 8;  
 Best Local Similarity 75.0%; Pred. No. 1.1e+05;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 NSWG 5  
 : : :  
 : : :  
 Db 5 SSWG 8

RESULT 16  
 CEP1\_ACHFU STANDARD; PRT; 11 AA.

AC P22790;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 01-DEC-1992 (Rel. 24, Last annotation update)  
 DE Cardio-excitatory peptide-1 (ACEP-1).  
 OS Achatina fulica (Giant African snail).  
 OS Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;  
 OC Achatinacea; Achatinidae; Achatina.  
 OC NCBI\_TaxID=6530;  
 RN [1]  
 RP SEQUENCE.

RC STRAIN=Ferrussac; TISSUE=Heart atrium;  
 RX MEDLINE=90011261; PubMed=2322251;  
 RA Fujimoto K., Ohta N., Yoshida M., Kubota I., Munekata Y., Kobayashi M.;  
 RA "A novel cardio-excitatory peptide isolated from the atria of the  
 RT African giant snail, Achatina fulica".  
 RL Biochem. Biophys. Res. Commun. 167:777-783(1990).  
 CC -1- FUNCTION: POTENTIATES THE BEAT OF THE VENTRICLE, AND HAS ALSO  
 CC EXCITATORY ACTIONS ON THE PENIS RETRACTOR MUSCLE, THE BUCCAL  
 CC MUSCLE AND THE IDENTIFIED NEURONS CONTROLLING THE BUCCAL MUSCLE  
 CC MOVEMENT OF ACHATINA.  
 CC -1- SIMILARITY: TO POSSIBLE PEPTIDE L5 FROM APLYSIA.  
 DR PIR: A34662; A34662.  
 KM Hormone; Amidation.  
 FT MOD.RES 11  
 FT MOD.RES 11 AA; 1305 MW; 82D6D5B9C7741365 CRC64;  
 SQ SEQUENCE

Query Match 24.7%; Score 22; DB 1; Length 11;  
 Best Local Similarity 57.1%; Pred. No. 8.4e+02;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 SWSGCR 9  
 : : :  
 : : :  
 Db 4 SWSRQGR 10

RESULT 17  
 LCK\_DROME STANDARD; PRT; 15 AA.

AC P81829;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Leucokinin (DLK).  
 GN PP OR DLK.  
 OS Drosophila melanogaster (Fruit fly).  
 CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
 CC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
 CC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
 OC NCBI\_TaxID=7227;  
 RN [1]



RP SEQUENCE.  
 RC TISSUE-Neurosecretory cell;  
 RX MEDLINE-20044845; PubMed-1054744;  
 RA Terhaz S., O'Connell F.C., Pollock V.P., Kean L., Davies S.A.,  
 RA Veenstra J.A., Dow J.A.T.;  
 RT Isolation and characterization of a leucokinin-like peptide of  
 RT Drosophila melanogaster;  
 RT J. Exp. Biol. 202;3667-3676(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-Berkeley;  
 RA Gelniker S.E., Agdayani A., Arcalina T.T., Baxter E., Blazek R.G.,  
 RA Butenkov C., Champe M., Chavez C., Chew M., Ciesiolka L., Doyle C.M.,  
 RA Farfan D.E., Galle R., George R.A., Harris N.L., Hoskins R.A.,  
 RA Houston K.A., Hummel S.R., Karia K., Kearney L., Kim E., Lee B.,  
 RA Lewis S., Li P., Lomolan M.A., Mazda P., Moshrefi A.R., Moshrefi A.,  
 RA Nixon R., Paclet J.M., Park S., Pfeiffer B., Poon L., Sequeira A.,  
 RA Sethi H., Smit E., Svirskas R.R., Wan K.H., Weinburg T., Zhang R.,  
 RA Ziehan L.L., Rubin G.M.;  
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: ACTS THROUGH INTRACELLULAR CALCIUM IN MALPIGHIAN TUBULE  
 CC STELLATE CELLS TO RAISE CHLORIDE CONDUCTANCE.  
 CC  
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 CC  
 CC EMBL: AC006496; NOT\_ANNOTATED\_CDS.  
 DR Flybase: FBgn028418; Leucokinin.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 15 15  
 SQ SEQUENCE 15 AA; 1743 MW; 4793A08E251C9525 CRC64;  
 OY 2 NSMG 5  
 DB 12 HSWG 15  
 RESULT 18  
 GOME\_ACAGO STANDARD; PRT; 18 AA.  
 AC P82358;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE GomeSin.  
 OS Acanthoscurria gomesiana.  
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;  
 OC Mygalomorphae; Theraphosidae; Acanthoscurria.  
 OX NCBI\_TaxID=115339;  
 RN [1]  
 RP SEQUENCE, MASS SPECTROMETRY, ACTIVITY, TISSUE SPECIFICITY, AMIDATION,  
 RP AND DISULFIDE BONDS.  
 RC TISSUE-Hemocyte;  
 RX MEDLINE-20517902; PubMed-10942757;  
 RA Silva P.J., Jr., Daffre S., Bulet P.;  
 RT "Isolation and characterization of gomesin, an 18-residue cysteine-  
 RT rich defense peptide from the spider Acanthoscurria gomesiana  
 RT hemocytes with sequence similarities to horseshoe crab antimicrobial  
 RT peptides of the tachyplesin family";  
 RL J. Biol. Chem. 275;33464-33470(2000).  
 CC -1- FUNCTION: ACTIVE AGAINST SEVERAL GRAM-POSITIVE BACTERIA SUCH AS  
 CC BACILLUS SPP., STAPHYLOCOCCUS SPP AND E.FAECALIS, SEVERAL GRAM-  
 CC NEGATIVE BACTERIA SUCH AS E.COLI, K.PNEUMONIAE, P.AERGINOSA AND  
 CC SALMONELLA SPP., FILAMENTOUS FUNGI SUCH AS N.CRASSA, T.VIRIDAE

CC AND YEASTS SUCH AS C.ALBICANS. IT IS ACTIVE AGAINST THE PARASITE  
 CC L.AMAZONENSIS AS WELL. IT SHOWS HEMOLYTIC ACTIVITY.  
 CC -1- TISSUE SPECIFICITY: HEMOCYTES.  
 CC -1- MASS SPECTROMETRY: MW=2270.4; METHOD-MALDI.  
 KW Amidation; Antibiotic; Fungicide; Hemolysis.  
 FT MOD\_RES 1 1  
 FT MOD\_RES 18 18  
 FT DISULFID 2 15  
 FT DISULFID 6 11  
 SQ SEQUENCE 18 AA; 2293 MW; 25ED499784908913 CRC64;  
 OY 6 CKGR 9  
 DB 15 CKGR 18  
 RESULT 19  
 SCX6\_TITBA STANDARD; PRT; 19 AA.  
 ID SCX6\_TITBA  
 AC P56610;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE Toxin Tbx-VI (Fragment).  
 OS Tityus bahiensis (Brazilian scorpion).  
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;  
 OC Buthoidea; Buthidae; Tityus.  
 OX NCBI\_TaxID=50343;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE-Venom;  
 RX MEDLINE-96190713; PubMed-8611151;  
 RA Becerril B., Corona M., Coronas F.I., Zamudio F.,  
 RA Calderon-Aranda E.S., Fletcher P.L., Jr., Martin B.M., Possant L.D.;  
 RT "Toxic peptides and genes encoding toxin gamma of the Brazilian  
 RT scorpions Tityus bahiensis and Tityus stigmurus";  
 RL Biochem. J. 313;753-760(1996).  
 CC -1- FUNCTION: NOT TOXIC IN MICE.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY.  
 CC ALPHA-TOXIN SUBFAMILY.  
 DR Interpro: IPR002061; Scorpion\_toxinL.  
 DR Pfam: PF00537; toxin\_3; 1.  
 FT NON\_TER 19 19  
 SQ SEQUENCE 19 AA; 2151 MW; 3535A2F1E5E67D14 CRC64;  
 OY 5 GCKGRITCY 13  
 DB 11 GCK-LTGF 17  
 RESULT 20  
 LEC3\_ARTIN STANDARD; PRT; 20 AA.  
 ID LEC3\_ARTIN  
 AC P18673;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 01-JUL-1993 (Rel. 26, Last annotation update)  
 DE Agglutinin beta-3 chain (Jaccalin beta-3 chain).  
 OS Artocarpus integer (Jack fruit) (Artocarpus integrifolia).  
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eucoside I; Rosales; Moraceae; Artocarpus.  
 OX NCBI\_TaxID=3490;  
 RN [1]  
 Query Match 24.7%; Score 22; DB 1; Length 19;  
 Best Local Similarity 44.4%; Pred. No. 1.4e+03;  
 Matches 4; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

RP SEQUENCE.  
RC TISSUE-Seed;  
RX MEDLINE-89206218; PubMed-2705782;  
RA Young N.M., Johnston R.A.Z., Szabo A.G., Watson D.C.;  
RT "Homology of the D-galactose-specific lectins from *Artocarpus integrifolia* and *MacLura pomifera* and the role of an unusual small polypeptide subunit.";  
RL Arch. Biochem. Biophys. 270:596-603(1989).  
RN [2]  
RP SEQUENCE.  
RX MEDLINE-92287028; PubMed-1599414;  
RA Mahanta S.K., Sanher S., Prasad Rao N.V.S.A.V., Swamy M.J.,  
RT "Primary structure of a Thomsen-Friedenreich-antigen-specific lectin, jacalin [*Artocarpus integrifolia* (jack fruit) agglutinin]. Evidence for the presence of an internal repeat.";  
RL Biochem. J. 284:95-101(1992).  
CC -1- FUNCTION: D-GALACTOSE-SPECIFIC LECTIN, BINDS THE T-ANTIGEN-STRUCTURE GAL-BETA1-3-GALNAc (THOMSEN-FRIEDENREICH-ANTIGEN-SPECIFIC LECTIN).  
CC -1- FUNCTION: POTENT AND SELECTIVE STIMULANT OF DISTINCT T- AND B-CELL FUNCTIONS. SHOWS A UNIQUE ABILITY TO SPECIFICALLY RECOGNIZE IGA-1 FROM HUMAN SERUM.  
CC -1- SUBUNIT: TETRAMER OF FOUR ALPHA CHAIN ASSOCIATED WITH TWO OR FOUR BETA CHAINS.  
CC -1- SIMILARITY: TO THE OTHER AGGLUTININ BETA CHAINS.  
DR PIR; S03985; S03985.  
KW Lectin; Iga-binding protein.  
SQ SEQUENCE 20 AA; 2058 MW; 894AFC989B0E212 CRC64;

Query Match 24.7%; Score 22; DB 1; Length 20;  
Best Local Similarity 75.0%; Pred. No. 1.4e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 MGCK 7  
Db 15 MGAK 18

RESULT 21  
LCR8\_LEUMA STANDARD; PRT; 8 AA.  
AC P19990;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 01-FEB-1991 (Rel. 17, Last annotation update)  
DE Leucokinin VIII (L-VIII).  
OS Leucophaea maderae (Madeira cockroach).  
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
OC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;  
OC Blaberidae; Blaberidae; Leucophaea.  
OX NCBI\_TaxID-6988;  
RN [1]  
RP SEQUENCE.  
RC TISSUE-Head;  
RA Holman G.M., Cook B.J., Nachman R.J.;  
RT "Isolation, primary structure and synthesis of leucokinin VII and VIII: the final members of this new family of cephalomyotropic peptides isolated from head extracts of *Leucophaea maderae*.";  
RL Comp. Biochem. Physiol. 88C:31-34(1987).  
CC -1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE ACTIVITY OF COCKROACH PROTODERM (HINDGUT).  
CC -1- SIMILARITY: TO THE OTHER LEUCOKININS.  
DR PIR; JS0318; JS0318.  
KW Neuropeptide; Amidation.  
FT MOD.RES 8  
SO SEQUENCE 8 AA; 902 MW; 736365AB9CADD8 CRC64;

Query Match 23.6%; Score 21; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.1e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 SMG 5

Db 6 SMG 8  
RESULT 22  
TACL\_TACGI STANDARD; PRT; 17 AA.  
AC P23684; 1991 (Rel. 20, Created)  
DT 01-NOV-1991 (Rel. 20, Last sequence update)  
DT 01-NOV-1991 (Rel. 32, Last annotation update)  
DE Tachyplesin I.  
OS Tachyplesus gigas (Southeast Asian horseshoe crab), and  
OS Carcinoscopus rotundicauda (Southeast Asian horseshoe crab).  
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;  
OC Limulidae; Tachyplesus.  
OX NCBI\_TaxID-6852; 6848;  
RN [1]  
RP SEQUENCE.  
RC SPECIES-T. gigas, and C. rotundicauda;  
RX MEDLINE-91035357; PubMed-2229025;  
RA Muta T., Fujimoto T., Nakajima H., Iwanaga S.;  
RT "Tachyplesins isolated from hemocytes of Southeast Asian horseshoe crabs (*Carcinoscopus rotundicauda* and *Tachyplesus gigas*): identification of a new tachyplesin, tachyplesin III, and a processing intermediate of its precursor.";  
RL J. Biochem. 108:261-266(1990).  
CC -1- SIMILARITY: BELONGS TO THE TACHYPLESIN/POLYPHEMUSIN FAMILY.  
DR PIR; A38824; A38824.  
KW PIR; JX0124; JX0124.  
KW Antibiotic; Amidation.  
FT DISULFID 3  
FT DISULFID 7  
FT MOD.RES 17  
SQ SEQUENCE 17 AA; 2269 MW; E9E09BD9D2923C94 CRC64;

Query Match 23.6%; Score 21; DB 1; Length 17;  
Best Local Similarity 80.0%; Pred. No. 1.8e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 9 RICY 13  
Db 9 RICY 13

RESULT 23  
TAC3\_TACGI STANDARD; PRT; 17 AA.  
AC P18252;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE Tachyplesin III.  
OS Tachyplesus gigas (Southeast Asian horseshoe crab).  
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;  
OC Limulidae; Tachyplesus.  
OX NCBI\_TaxID-6852;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE-91035357; PubMed-2229025;  
RA Muta T., Fujimoto T., Nakajima H., Iwanaga S.;  
RT "Tachyplesins isolated from hemocytes of Southeast Asian horseshoe crabs (*Carcinoscopus rotundicauda* and *Tachyplesus gigas*): identification of a new tachyplesin, tachyplesin III, and a processing intermediate of its precursor.";  
RL J. Biochem. 108:261-266(1990).  
CC -1- FUNCTION: SIGNIFICANTLY INHIBITS THE GROWTH OF GRAM-NEGATIVE AND GRAM-POSITIVE BACTERIA.  
CC -1- TISSUE SPECIFICITY: HEMOCYTES.  
CC -1- SIMILARITY: BELONGS TO THE TACHYPLESIN/POLYPHEMUSIN FAMILY.  
DR PIR; JX0125; JX0125.  
KW Antibiotic; Amidation.  
FT DISULFID 3  
BY SIMILARITY. 16

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FT DISULFID 7 12 BY SIMILARITY.
MOD.RES 17 17 AMIDATION.
SQ SEQUENCE 17 AA; 2241 MW; E9E08CE9D2923C94 CRC64;

Query Match
Best Local Similarity 23.6%; Score 21; DB 1; Length 17;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 9 RICCY 13
DB 9 RGICY 13

RESULT 24
CXIL_CONMR STANDARD; PRT; 11 AA.
AC P58807;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
OS Lambda-conotoxin CMVIA.
OC Conus marmoreus (Marble cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conidae; Conus.
OX NCBI_TaxID=42752;
RN [1]
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RX TISSUE-Venom.
RX MEDLINE=20564325; PubMed=10988292;
RA Balaaji R.A., Ohtake A., Sato K., Gopalakrishnakone P., Kini R.M.,
RA Sew K.T., Bay B.-H.;
RT "Lambda-conotoxins, a new family of conotoxins with unique disulfide
RT pattern and protein folding. Isolation and characterization from the
RL venom of Conus marmoreus."
CC J. Biol. Chem. 275:39516-39522(2000).
CC -1- FUNCTION: Inhibits the neuronal noradrenergic transporter.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- MASS SPECTROMETRY: MW=1237.93; MW_ERR=0.21; METHOD=Electrospray.
CC -1- SIMILARITY: BELONGS TO THE CHI/LAMBDA-CONOTOXIN FAMILY.
KW Neurotoxin; Toxin; Hydroxylation.
FT DISULFID 2 11
FT MOD.RES 10 10 HYDROXYLATION.
SQ SEQUENCE 11 AA; 1226 MW; 277AAC60B233B58 CRC64;

Query Match
Best Local Similarity 22.5%; Score 20; DB 1; Length 11;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 6 CKGRICY 13
DB 2 CCGYKICH 9

RESULT 25
TIN3_HOPTI
ID TIN3_HOPTI STANDARD; PRT; 12 AA.
AC P82653;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
OS Tigerlilyin-3.
OC Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae;
OC Hoplobatrachus.
OX NCBI_TaxID=103373;
RN [1]
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.
RC TISSUE-Skin;
AC PubMed=11031261;
RA Purna Sai K., Jagannathan M.V., Vairaman M., Raju N.P.,

RA Devi A.S., Nagaraj R., Sitaram N.;
RT "Tigerlilyins: novel antimicrobial peptides from the Indian frog Rana
RT tigerina."
RL J. Biol. Chem. 276:2701-2707(2001).
CC -1- FUNCTION: ANTIACETABULAR ACTIVITY AGAINST B. SUBTILIS, E. COLI,
CC S. AUREUS, M. LUTENS, P. PUTIDA AND S. CEREVISIAE.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: SKIN.
CC -1- MASS SPECTROMETRY: MW=1409; METHOD=MALDI.
KW Amphibian skin; Antibiotic; Amidation.
FT DISULFID 3 11
FT MOD.RES 12 12 AMIDATION.
SQ SEQUENCE 12 AA; 1411 MW; C0717DBED37605D CRC64;

Query Match
Best Local Similarity 22.5%; Score 20; DB 1; Length 12;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 ICY 13
DB 10 ICY 12

RESULT 26
CXIL_CONMR STANDARD; PRT; 13 AA.
AC P58810;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
OS Lambda/chi-conotoxin M7B (Chi-M7B).
OC Conus marmoreus (Marble cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conidae; Conus.
OX NCBI_TaxID=42752;
RN [1]
RP SEQUENCE, SYNTHESIS, AND STRUCTURE BY NMR.
RX TISSUE-Venom;
RX MEDLINE=21419681; PubMed=11528421;
RA Sharpe I.A., Gehrmann J., Loughnan M.L., Thomas L., Adams D.A.,
RA Atkins A., Palant E., Craik D.J., Adams D.J., Alewood P.F.,
RA Lewis R.J.;
RT "Two new classes of conopeptides inhibit the alpha1-adrenoceptor and
RT noradrenergic transporter."
RL Nat. Neurosci. 4:902-907(2001).
CC -1- FUNCTION: Inhibits the neuronal noradrenergic transporter.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- PTM: Exists in two forms, due to cis-trans isomerization at His-
CC 11-Hyp-12.
CC -1- MASS SPECTROMETRY: MW=1393.52; METHOD=Electrospray.
CC -1- SIMILARITY: BELONGS TO THE CHI/LAMBDA-CONOTOXIN FAMILY.
DR PDB: 1IEO; 03-APR-02.
KW Neurotoxin; Toxin; Hydroxylation; 3D-structure.
FT DISULFID 4 13
FT MOD.RES 12 12 HYDROXYLATION.
SQ SEQUENCE 13 AA; 1382 MW; 277AAC376EAD2B58 CRC64;

Query Match
Best Local Similarity 22.5%; Score 20; DB 1; Length 13;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 6 CKGRICY 13
DB 4 CCGYKICH 11

RESULT 27
SMS1_MYOSC
ID SMS1_MYOSC STANDARD; PRT; 14 AA.
AC P20750;
RA 01-FEB-1991 (Rel. 17, Created)

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01-FEB-1991 (Rel. 17, Last sequence update)  
 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Somatostatin I.  
 OS Myoxocephalus scorpius (Shorthorn sculpin) (Daddy sculpin),  
 OS Oncorhynchus kisutch (coho salmon), and  
 OS Anguilla anguilla (European freshwater eel).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes;  
 OC Cottidae; Cottidae; Myoxocephalus.  
 OC NCBI\_Taxid=8097, 8019, 7936;  
 RN [1]  
 RP SEQUENCE.  
 RC SPECIES=M. scorpius; TISSUE=Pancreas;  
 RX MEDLINE=88029486; PubMed=2889597;  
 RA Conlon J.M., Davis M.S., Falkner S., Thim L.;  
 RT "Structural characterization of peptides derived from  
 RT prosomatostatin I and II isolated from the pancreatic islets of two  
 RT species of teleostean fish: the daddy sculpin and the flounder.";  
 RL Eur. J. Biochem. 168:647-652(1987).  
 RN [2]  
 RP SEQUENCE.  
 RC SPECIES=O. kisutch; TISSUE=Pancreas;  
 RX MEDLINE=87055212; PubMed=2877919;  
 RA Pletsch-Kaya E.M., Pollock H.G., Rouse J.B., Hamilton J.W.,  
 RA Kimmel J.R., Andrews P.C., Gorman A.;  
 RT "Characterization of coho salmon (Oncorhynchus kisutch) islet  
 RT somatostatins.";  
 RL Gen. Comp. Endocrinol. 63:252-263(1986).  
 RN [3]  
 RP SEQUENCE.  
 RC SPECIES=A. anguilla; TISSUE=Pancreas;  
 RX MEDLINE=89065329; PubMed=2904391;  
 RA Conlon J.M., Deacon C.F., Hazon N., Henderson I.W., Thim L.;  
 RT "Somatostatin-related and glucagon-related peptides with unusual  
 RT structural features from the European eel (Anguilla anguilla).";  
 RL Gen. Comp. Endocrinol. 72:181-189(1988).  
 CC -1- FUNCTION: SOMATOSTATIN INHIBITS THE RELEASE OF SOMATOTROPIN.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: BELONGS TO THE SOMATOSTATIN FAMILY.  
 DR PIR: S00172; S00172.  
 DR PIR: B60842; B60842.  
 DR PIR: A60840; A60840.  
 DR InterPro: IPR004250; Somatostatin.  
 DR Pfam: PF03002; Somatostatin; 1.  
 KW Hormone; Multigene family.  
 FT DISULFID 3  
 FT DISULFID 14  
 SQ SEQUENCE 14 AA; 1640 MW; D6270F5C09682679 CRC64;  
 Query Match 22.5%; Score 20; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RC SPECIES=A. mississippiensis; TISSUE=Stomach;  
 RX MEDLINE=93324451; PubMed=8101369;  
 RA Wang Y., Conlon J.M.;  
 RT "Neuroendocrine peptides (NPY, GRP, VIP, somatostatin) from the brain  
 RT and stomach of the alligator.";  
 RL Peptides 14:573-579(1993).  
 RN [2]  
 RP SEQUENCE.  
 RC SPECIES=T. scripta;  
 RX MEDLINE=90341082; PubMed=1974347;  
 RA Conlon J.M., Hicks J.W.;  
 RT "Isolation and structural characterization of insulin, glucagon and  
 RT somatostatin from the turtle, Pseudemys scripta.";  
 RL Peptides 11:461-466(1990).  
 CC -1- FUNCTION: SOMATOSTATIN INHIBITS THE RELEASE OF SOMATOTROPIN.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: BELONGS TO THE SOMATOSTATIN FAMILY.  
 DR PIR: G60414; G60414.  
 DR InterPro: IPR004250; Somatostatin.  
 DR Pfam: PF03002; Somatostatin; 1.  
 KW Hormone.  
 FT DISULFID 3  
 FT DISULFID 14  
 SQ SEQUENCE 14 AA; 1640 MW; D6270F5C09682679 CRC64;  
 Query Match 22.5%; Score 20; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 29  
 CX1B CONBE STANDARD; PRT; 15 AA.  
 ID CX1B CONBE  
 AC P58624;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Conotoxin BetylXb.  
 OS Conus betulinus (Beech cone).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
 OC Neogastropoda; Conoidea; Conidae; Conus.  
 OC NCBI\_Taxid=89764;  
 RN [1]  
 RP SEQUENCE AND MASS SPECTROMETRY.  
 RC TISSUE=Venom;  
 RX MEDLINE=20058566; PubMed=10591037;  
 RA Chen J.-S., Fan C.-X., Hu K.-P., Wei K.-H., Zhong M.-N.;  
 RT "Studies on conotoxins of Conus betulinus.";  
 RL J. Nat. Toxins 8:341-349(1999).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.  
 CC -1- MASS SPECTROMETRY: MW=1642.5; METHOD=MALDI.  
 CC -1- SIMILARITY: BELONGS TO THE M-SUPERFAMILY OF CONOTOXINS.  
 KW Neurotoxin; Toxin.  
 FT DISULFID 1  
 FT DISULFID 2  
 FT DISULFID 6  
 FT DISULFID 12  
 FT DISULFID 13  
 FT DISULFID 15  
 SQ SEQUENCE 15 AA; 1650 MW; 3749BAF08E311337 CRC64;  
 Query Match 22.5%; Score 20; DB 1; Length 15;  
 Best Local Similarity 42.9%; Pred. No. 2.3e+03;  
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

RESULT 30  
 ISOL\_CYPCA  
 QY 6 CKRRIIC 12  
 DB 6 CHGCVPC 12

ID ISOT\_CYPCA STANDARD; PRT: 9 AA.  
AC P42993;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE Isotocin.  
OS Cyprinus carpio (Common carp).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Cyprinus.  
OX NCBI\_TaxID=7962;  
RN [1]  
RP SEQUENCE  
RC TISSUE=Pituitary;  
RA Achet R., Chauvet J., Chauvet M.-T., Crepy D.;  
RT "Characterization of neurohypophyseal hormones from a fresh water bony  
RT fish, the carp (Cyprinus carpio). Comparison with hormones from sea  
RT water bony fish."  
RL Comp. Biochem. Physiol. 14:245-254(1965).  
CC -1- FUNCTION: ANTIDIURETIC HORMONE.  
CC -1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.  
DR PIR; A61364; A61364.  
DR InterPro: IPR000981; Neurhyp\_horm.  
DR InterPro: IPR001230; Prenyl\_site.  
DR Pfam: PF00220; hormone4.1.  
DR PROSITE: PS00264; NEUROHYPOPHYS\_HORM; 1.  
KW Hormone; Amidation.  
FT DISUFID 1 6  
FT MOD\_RES 9 9  
SQ SEQUENCE 9 AA; 969 MW; 17FF476EB455B04B CRC64;  
  
Query Match 21.3%; Score 19; DB 1; Length 9;  
Best Local Similarity 75.0%; Pred. No. 1.1e+05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 12 CYTS 15  
DB 1 1  
1 CYIS 4

Search completed: June 5, 2003, 08:59:40  
Job time : 13 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 5, 2003, 08:58:43 ; Search time 27 Seconds  
(without alignments)  
114.471 Million cell updates/sec

Title: US-09-605-573a-69\_COPY\_12-26  
Perfect score: 89  
Sequence: 1 LNSWCKGRITCYTS 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 6395

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database :  
1: SP archaea:\*  
2: SP bacteria:\*  
3: SP fungi:\*  
4: SP human:\*  
5: SP invertebrate:\*  
6: SP mammal:\*  
7: SP mhc:\*  
8: SP organelle:\*  
9: SP phage:\*  
10: SP plant:\*  
11: SP rodent:\*  
12: SP virus:\*  
13: SP vertebrate:\*  
14: SP unclassified:\*  
15: SP viirus:\*  
16: SP bacteriap:\*  
17: SP archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	30.3	8	5	P82685 periplaneta
2	27	30.3	8	5	P82687 periplaneta
3	27	30.3	8	5	P82689 periplaneta
4	27	30.3	17	6	O9Y0Z5 O9Y0Z5
5	27	30.3	20	10	O9S871 O9S871
6	25	28.1	15	12	O66543 O66543
7	25	28.1	15	12	O66543 O66543
8	24.5	27.5	20	13	O9DE23 O9DE23
9	24	27.0	12	15	O12036 O12036
10	24	27.0	17	3	O06800 saccharomyc
11	24	27.0	20	10	O9X1W8 O9X1W8
12	24	27.0	20	10	O9S8E0 O9S8E0
13	24	27.0	20	11	O9O0U8 O9O0U8
14	24	27.0	20	12	O84861 O84861
15	23	25.8	10	2	O50032 O50032
16	23	25.8	12	7	O31006 O31006

17	23	25.8	16	2	O45663	O45663 bacillus su
18	23	25.8	18	4	O96C65	O96C65 homo sapien
19	22	24.7	8	5	P82686	P82686 periplaneta
20	22	24.7	8	5	P82688	P82688 periplaneta
21	22	24.7	11	7	O77914	O77914 oreochromis
22	22	24.7	12	2	O56947	O56947 yersinia ps
23	22	24.7	13	2	O52920	O52920 rhizobium m
24	22	24.7	13	8	O9X1I2	O9X1I2 bentisia tab
25	22	24.7	15	2	O69142	O69142 streptococc
26	22	24.7	16	11	O9OV10	O9OV10 mus sp. mep
27	22	24.7	16	13	O9P8P0	O9P8P0 oryzias lat
28	22	24.7	17	11	O8V157	O8V157 mus musculu
29	22	24.7	20	2	O93TWO	O93TWO neisseria m
30	22	24.7	12	12	O66202	O66202 transmissib
31	21	23.6	14	2	P83077	P83077 bacillus ce
32	21	23.6	15	6	O9RS39	O9RS39 gotilla gor
33	21	23.6	15	6	O9TRP3	O9TRP3 sus scrofa
34	21	23.6	15	13	O9PS01	O9PS01 microgogni
35	21	23.6	16	2	O44543	O44543 anabaena va
36	21	23.6	16	4	O16183	O16183 homo sapien
37	21	23.6	17	2	O93S31	O93S31 rhodospiril
38	21	23.6	17	12	O85004	O85004 porcine res
39	21	23.6	18	4	O13665	O13665 homo sapien
40	21	23.6	18	17	O9UYK7	O9UYK7 pyrococcus
41	21	23.6	19	2	P74875	P74875 salmoneila
42	21	23.6	19	11	O06028	O06028 mus musculu
43	21	23.6	20	13	O9PRR4	O9PRR4 scyllorhinu
44	21	23.6	16	13	O9PRY2	O9PRY2 scyllorhinu
45	20.5	23.0	10	4	O9P229	O9P229 petromyzon
46	20	22.5	10	8	O8WD18	O8WD18 homo sapien
47	20	22.5	10	8	O8W804	O8W804 anolis tran
48	20	22.5	10	8	O8W804	O8W804 anolis punc
49	20	22.5	10	8	O8W803	O8W803 anolis nite
50	20	22.5	10	8	O8W802	O8W802 anolis punc
51	20	22.5	10	10	P82938	P82938 hordeum vul
52	20	22.5	11	6	O9TRX2	O9TRX2 bos taurus
53	20	22.5	11	7	O78118	O78118 oreochromis
54	20	22.5	11	7	O78120	O78120 oreochromis
55	20	22.5	11	7	O9G682	O9G682 chelosania
56	20	22.5	12	7	O77889	O77889 oreochromis
57	20	22.5	12	7	O77890	O77890 oreochromis
58	20	22.5	12	7	O77891	O77891 oreochromis
59	20	22.5	12	7	O77920	O77920 pseudotroph
60	20	22.5	13	4	O14890	O14890 homo sapien
61	20	22.5	13	6	O9TRX1	O9TRX1 bos sapien
62	20	22.5	14	2	O43905	O43905 azospirilla
63	20	22.5	15	4	O9BQ58	O9BQ58 nitrosomona
64	20	22.5	15	4	O9BQ73	O9BQ73 homo sapien
65	20	22.5	15	6	O9BQ73	O9BQ73 homo sapien
66	20	22.5	15	11	O9OUR7	O9OUR7 sus scrofa
67	20	22.5	16	4	O15632	O15632 mus sp. giu
68	20	22.5	16	10	O9S8C0	O9S8C0 lupinus alb
69	20	22.5	16	11	O15276	O15276 homo sapien
70	20	22.5	17	4	O15276	O15276 homo sapien
71	20	22.5	18	4	O9UCN1	O9UCN1 homo sapien
72	20	22.5	19	4	O9UCN1	O9UCN1 homo sapien
73	20	22.5	19	10	O9S8J3	O9S8J3 trichosanthe
74	20	22.5	20	5	O9GPR4	O9GPR4 homo sapien
75	20	22.5	20	10	O9S8J1	O9S8J1 trichosanthe
76	20	22.5	20	11	P97907	P97907 mus musculu
77	20	22.5	20	11	O9OUY9	O9OUY9 mus musculu
78	20	22.5	20	3	O9URC1	O9URC1 phaneroche
79	19.5	21.9	20	3	O9URC1	O9URC1 human adeno
80	19	21.3	12	12	O9TEZ9	O9TEZ9 human adeno
81	19	21.3	12	12	O9TEZ9	O9TEZ9 human adeno
82	19	21.3	13	15	O92820	O92820 chimpanzee
83	19	21.3	15	6	O9TRN8	O9TRN8 sus scrofa
84	19	21.3	15	11	O9QW89	O9QW89 ratius sp.
85	19	21.3	15	15	O9Q045	O9Q045 chimpanzee
86	19	21.3	17	8	O03888	O03888 chlorogoni
87	19	21.3	18	4	O14042	O14042 homo sapien
88	19	21.3	18	5	O9WPF2	O9WPF2 pheretima v
89	19	21.3	18	8	O34695	O34695 homarus ame

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90 19 21.3 19 11 Q8VCM9 08vcm9 mus musculi
91 19 21.3 20 2 Q9R502 09r502 thermotoga
92 19 21.3 20 2 Q9R4Y1 09r4y1 proteus vul
93 19 21.3 20 6 Q9TO08 09tq08 oryctolagus
94 19 21.3 20 6 Q9TRH8 09trh8 oryctolagus
95 19 21.3 20 10 Q9SEC3 09sec3 lupinus alb
96 19 21.3 20 11 Q9JLV2 09jlv2 mus musculi
97 19 21.3 20 11 Q9QUL9 09qul9 rattus sp.
98 19 21.3 20 11 Q9QUL8 09qul8 rattus sp.
99 19 21.3 20 11 Q8RI01 08ri01 mus musculi
100 19 21.3 20 15 Q9DYR0 09dyr0 human immun

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## ALIGNMENTS

```

RESULT 1
P82685 PRELIMINARY: PRT: 8 AA.
ID P82685;
AC P82685;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
DE 01-MAR-2001 (TREMBLrel. 16, last annotation update)
DE Kinn-1 (PEA-K-1).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattodea; Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=CORPORA CARDIACA;
RX MEDLINE=98010462; PubMed=9350979;
RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of eight kins from the
RT retrocerebral complex of the American cockroach, Periplaneta
RT americana."
RT Regul. Pept. 71:199-205(1997).
CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -1- SIMILARITY: BELONGS TO THE KININ FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 8 AA; 950 MW; 326365B449D5A774 CRC64;
SQ SEQUENCE 8 AA; 950 MW; 326365B449D5A774 CRC64;

Query Match 30.3%; Score 27; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 NSWG 5
DB 5 NSWG 8

RESULT 2
P82687 PRELIMINARY: PRT: 8 AA.
ID P82687;
AC P82687;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
DE 01-MAR-2001 (TREMBLrel. 16, last annotation update)
DE Kinn-3 (PEA-K-3).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattodea; Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=CORPORA CARDIACA;
RX MEDLINE=98010462; PubMed=9350979;
RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of eight kins from the

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RT retrocerebral complex of the American cockroach, Periplaneta
RT americana."
RT Regul. Pept. 71:199-205(1997).
CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -1- SIMILARITY: BELONGS TO THE KININ FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 8 AA; 909 MW; DC6365B449D5A76A CRC64;
SQ SEQUENCE 8 AA; 909 MW; DC6365B449D5A76A CRC64;

Query Match 30.3%; Score 27; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 NSWG 5
DB 5 NSWG 8

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RESULT 3
P82689 PRELIMINARY: PRT: 8 AA.
ID P82689;
AC P82689;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
DE 01-MAR-2001 (TREMBLrel. 16, last annotation update)
DE Kinn-5 (PEA-K-5).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattodea; Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=CORPORA CARDIACA;
RX MEDLINE=98010462; PubMed=9350979;
RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of eight kins from the
RT retrocerebral complex of the American cockroach, Periplaneta
RT americana."
RT Regul. Pept. 71:199-205(1997).
CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -1- SIMILARITY: BELONGS TO THE KININ FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 8 AA; 865 MW; C76365B449D5A775 CRC64;
SQ SEQUENCE 8 AA; 865 MW; C76365B449D5A775 CRC64;

Query Match 30.3%; Score 27; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 NSWG 5
DB 5 NSWG 8

RESULT 4
Q9TQZ5 PRELIMINARY: PRT: 17 AA.
ID Q9TQZ5;
AC Q9TQZ5;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, last annotation update)
DE Glyceraldehyde 3-phosphate dehydrogenase (Fragmant).
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE.
RC MEDLINE=96273610; PubMed=8690030;

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RA Nicolas M.G., Fujiki K., Murayama K., Suzuki M.T., Mineki R.,  
 RA Hayakawa M., Yoshikawa Y., Cho F., Kanai A.;  
 RT "Studies on the mechanism of early onset macular degeneration in  
 RT cynomolgus (Macaca fascicularis) monkeys. I. Abnormal concentrations  
 of two proteins in the retina."  
 RL Exp. Eye Res. 62:211-219(1996).  
 CC -1- CATALYTIC ACTIVITY: D-GLYCERALDEHYDE 3-PHOSPHATE + PHOSPHATE +  
 CC NAD(+) = 3-PHOSPHO-D-GLYCEROYL PHOSPHATE + NADH.  
 CC -1- SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE  
 CC DEHYDROGENASE FAMILY.  
 DR InterPro: IPR000173; GAP\_dhdrogenase.  
 DR Pfam: PF000044; gpdh; 1.  
 KW Glycolysis; NAD; Oxidoreductase.  
 SQ SEQUENCE 17 AA; 1671 MW; 52CCDD0D1A98B3DAF CRC64;

Query Match 30.3%; Score 27; DB 6; Length 17;  
 Best Local Similarity 36.4%; Pred. No. 6.4e+02;  
 Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
 Oy 1 LNSMCKGRIT 11  
 Db 7 VNGFGAIGRLV 17

RESULT 5  
 O9S8T1 PRELIMINARY; PRT; 20 AA.  
 AC O9S8T1; 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Jacalin beta-subunit (Fragment).  
 OS Artocarpus tonkinensis.  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 CC Eucosids I; Rosales; Moraceae; Artocarpus.  
 OX NCBI\_TaxID=3492;  
 RN 1  
 RP MEDLINE=93152601; PubMed=8427879;  
 RA Ngoc L.D., Brillard M., Hoebke J.;  
 RT "The alpha- and beta-subunits of the jacalins are cleavage products  
 RT from a 17-kDa precursor."  
 RL Biochim. Biophys. Acta 1156:219-222(1993).  
 FT NON\_TER 1  
 FT NON\_TER 1  
 SQ SEQUENCE 20 AA; 2131 MW; 894893667060EFFF CRC64;

Query Match 30.3%; Score 27; DB 10; Length 20;  
 Best Local Similarity 57.1%; Pred. No. 7.6e+02;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 1 LNSMCKG 7  
 Db 12 VGSWMAK 18  
 ID 066543 PRELIMINARY; PRT; 15 AA.  
 AC 066543; 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)  
 DE Epitope C11 (16 AA) (Fragment)  
 OS Human herpesvirus 4 (Epstein-Barr virus).  
 CC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 CC Gammaherpesvirinae; Lymphocryptovirus.  
 OX NCBI\_TaxID=10376;  
 RN 1  
 RP MEDLINE=88296424; PubMed=2841116;  
 RC STRAIN=B95-8;  
 RX MEDLINE=88296424; PubMed=2841116;

RA Walls D., Gannon F.;  
 RT "The expression of novel antigens from the Epstein-Barr virus large  
 RT internal repeat."  
 RL EMBO J. 7:1191-1196(1988).  
 DR EMBL: X07814; CAA30673.1; -.  
 FT NON\_TER 1  
 FT NON\_TER 1  
 SQ SEQUENCE 15 AA; 1629 MW; 48BA5A4558C3266C CRC64;

Query Match 28.1%; Score 25; DB 12; Length 15;  
 Best Local Similarity 66.7%; Pred. No. 1.2e+03;  
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Oy 4 WGCKGR 9  
 Db 6 WGRKG 11

RESULT 7  
 O86576 PRELIMINARY; PRT; 15 AA.  
 AC O86576; 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Coat protein (Fragment).  
 OS Subterranean clover stunt virus.  
 CC Viruses; ssDNA viruses; Nanovirus.  
 OX NCBI\_TaxID=36772;  
 RN 1  
 RP MEDLINE=93212590; PubMed=8460528;  
 RA Chu P.W., Reese P., Qiu B.S., Waterhouse P.M., Gerlach W.L.;  
 RT "Putative full-length clones of the genomic DNA segments of  
 RT subterranean clover stunt virus and identification of the segment  
 RT coding for the viral coat protein."  
 RL Virus Res. 27:161-171(1993).  
 DR EMBL: S57687; AAB25908.1; -.  
 FT NON\_TER 1  
 FT NON\_TER 1  
 SQ SEQUENCE 15 AA; 1825 MW; 44D9CE497CD96FFD CRC64;

Query Match 28.1%; Score 25; DB 12; Length 15;  
 Best Local Similarity 80.0%; Pred. No. 1.2e+03;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 4 WGCKG 8  
 Db 5 WGRKG 9  
 ID 09DE23 PRELIMINARY; PRT; 20 AA.  
 AC 09DE23; 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE UORF2.  
 OS Gallus gallus (Chicken).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OX NCBI\_TaxID=9031;  
 RN 1  
 RP MEDLINE=20528616; PubMed=11073974;  
 RX Kodayashi M., Yu R.T., Yasuda K., Umesono K.;  
 RT "Cell-type-specific regulation of the retinoic acid receptor mediated  
 RT by the orphan nuclear receptor TLX."  
 RL Mol. Cell. Biol. 20:8731-8739(2000).  
 DR EMBL: AF220160; AAG35363.1; -.  
 DR InterPro: IPR000345; CytC\_heme\_bind.



090UK8  
ID 090UK8 PRELIMINARY: PRT: 20 AA.  
AC 090UK8;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-NOV-1996 (TREMBlrel. 13, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE Alpha class glutathione S-transferase subunit 1B (EC 2.5.1.18) (Fragment).  
OS Rattus sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
NC NCBL\_TaxID=10118;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=96036981; PubMed=7485987;  
RA Roullet P., Debrauwer L., Tulliez J.;  
RT Electrospray ionization-mass spectrometry as a tool for  
RT characterization of glutathione S-transferase isozymes.;  
DR Anal. Biochem. 229:304-312(1995).  
DR HSPF: P08263; IGUH.  
SQ SEQUENCE 20 AA; 2421 MW; 949F405B7DA0B236 CRC64;

Query Match 27.0%; Score 24; DB 11; Length 20;  
Best Local Similarity 33.3%; Pred. No. 2.4e+03;  
Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 1 LNSGCKGRITC 12  
Db 6 LHYFNAGRMGC 17  
ID 084861 PRELIMINARY: PRT: 20 AA.  
AC 084861;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE Hypothetical 2.2 kDa protein (Fragment).  
OS Unidentified human poliovirus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae; Enterovirus.  
OX NCBL\_TaxID=40278;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=87169734; PubMed=3031313;  
RA Kuge S., Saito I., Nomoto A.;  
RT "Primary structure of poliovirus defective-interfering particle  
RT genomes and possible generation mechanisms of the particles.";  
RL J. Mol. Biol. 192:473-487(1986).  
DR EMBL: M30218; AAA66827.1; -.  
KW Hypothetical protein.  
FT NON\_TER 1  
FT NON\_TER 20  
SQ SEQUENCE 20 AA; 2241 MW; 55D177D10BAF0F9 CRC64;

Query Match 27.0%; Score 24; DB 12; Length 20;  
Best Local Similarity 75.0%; Pred. No. 2.4e+03;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 NSNG 5  
Db 7 NNMG 10  
ID 050032 PRELIMINARY: PRT: 10 AA.  
AC 050032;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-NOV-1996 (TREMBlrel. 01, Last annotation update)  
DE U22669.

OS Mycobacterium leprae.  
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
OX NCBL\_TaxID=1769;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Smith D.R.;  
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA ROBISON K.;  
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.  
DR EMBL: U15182; AAA62975.1; -.  
SQ SEQUENCE 10 AA; 1137 MW; 5F3F317B1EB455B7 CRC64;

Query Match 25.8%; Score 23; DB 2; Length 10;  
Best Local Similarity 60.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 6 CKGR 10  
Db 6 CEGRL 10  
ID 031006 PRELIMINARY: PRT: 12 AA.  
AC 031006;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE Beta protein (Fragment).  
GN BOFA.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBL\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93052564; PubMed=1428011;  
RA Ellis S.A., Braem K.A., Morrison W.I.;  
RT "Transmembrane and cytoplasmic domain sequences demonstrate at least  
RT two expressed bovine MHC class I loci.";  
RL Immunogenetics 37:49-56(1992).  
DR EMBL: S47738; AAB23972.1; -.  
FT NON\_TER 1  
FT NON\_TER 12  
SQ SEQUENCE 12 AA; 1306 MW; 6D9E2F805ABB5044 CRC64;

Query Match 25.8%; Score 23; DB 7; Length 12;  
Best Local Similarity 70.0%; Pred. No. 2.2e+03;  
Matches 7; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

OY 5 GCKGRITCYT 14  
Db 1 GCKGRIT--YT 8  
ID 045663 PRELIMINARY: PRT: 16 AA.  
AC 045663;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)  
DE SacB levansucrase.  
OS Bacillus subtilis.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;  
OC Bacillaceae; Bacillus.  
OX NCBL\_TaxID=1423;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MARBURG;

RX MEDLINE=85295507; PubMed-2993818;  
 RA Steinmetz M., Le Cog D., Aymeric S., Gonzy-Treboul G., Gay P.;  
 RT "The DNA sequence of the gene for the secreted Bacillus subtilis  
 RT enzyme levanucrase and its genetic control sites.";  
 RL Mol. Gen. Genet. 200;220-228(1985).  
 DR EMBL; X02730; CAA26512.1; -;  
 SQ SEQUENCE 16 AA; 1840 MW; E8CF83DC73713DA9 CRC64;

Query Match 25.8%; Score 23; DB 2; Length 16;  
 Best Local Similarity 37.5%; Pred. No. 2.9e+03;  
 Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 6 CKGRITCY 13  
 DB 2 CKGOSYVF 9

## RESULT 18

ID 096C65 PRELIMINARY; PRT; 18 AA.  
 AC 096C65;  
 DT 01-DEC-2001 (TREMblrel. 19, Created)  
 DT 01-DEC-2001 (TREMblrel. 19, last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, last annotation update)  
 DE Hypothetical 2.1 kDa protein (Fragment).  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=EYE;  
 RA Strausberg R.;  
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC014643; AA014643.1; -;  
 KW Hypothetical protein.  
 FT NON TPR 1  
 SQ SEQUENCE 18 AA; 2105 MW; 3874A0D25D91AC9C CRC64;

Query Match 25.8%; Score 23; DB 4; Length 18;  
 Best Local Similarity 60.0%; Pred. No. 3.2e+03;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNSWG 5  
 DB 1 LDANG 5

## RESULT 19

ID P82686 PRELIMINARY; PRT; 8 AA.  
 AC P82686;  
 DT 01-MAR-2001 (TREMblrel. 16, Created)  
 DT 01-MAR-2001 (TREMblrel. 16, last sequence update)  
 DT 01-MAR-2001 (TREMblrel. 16, last annotation update)  
 DE Kinin-2 (PEA-K-2).  
 OS Periplaneta americana (American cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;  
 OC Blattellidae; Blattidae; Periplaneta.  
 OX NCBI\_Taxid=6978;  
 RN [1]  
 RP SEQUENCE, AND FUNCTION.  
 RC TISSUE=CORPORA CARDIACA;  
 RA MEDLINE=98010462; PubMed-9350979;  
 RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;  
 RT "Isolation and structural elucidation of eight kinins from the  
 RT retrocerebral complex of the American cockroach, Periplaneta  
 RT americana.";  
 RL Regul. Pept. 71:199-205(1997).  
 CC -I- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY  
 CC -I- (MYOTROPIC ACTIVITY).  
 CC -I- SIMILARITY: BELONGS TO THE KININ FAMILY.

KW Neuropeptide; Amidation.  
 FT MOD\_RES 8  
 SQ SEQUENCE 8 AA; 856 MW; DC6365A5B9DBDDA CRC64;

Query Match 24.7%; Score 22; DB 5; Length 8;  
 Best Local Similarity 75.0%; Pred. No. 6.7e+05;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 NSWG 5  
 DB 5 SSWG 8

## RESULT 20

ID P82688 PRELIMINARY; PRT; 8 AA.  
 AC P82688;  
 DT 01-MAR-2001 (TREMblrel. 16, Created)  
 DT 01-MAR-2001 (TREMblrel. 16, last sequence update)  
 DT 01-MAR-2001 (TREMblrel. 16, last annotation update)  
 DE Kinin-4 (PEA-K-4).  
 OS Periplaneta americana (American cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;  
 OC Blattellidae; Blattidae; Periplaneta.  
 OX NCBI\_Taxid=6978;  
 RN [1]  
 RP SEQUENCE, AND FUNCTION.  
 RC TISSUE=CORPORA CARDIACA;  
 RA MEDLINE=98010462; PubMed-9350979;  
 RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;  
 RT "Isolation and structural elucidation of eight kinins from the  
 RT retrocerebral complex of the American cockroach, Periplaneta  
 RT americana.";  
 RL Regul. Pept. 71:199-205(1997).  
 CC -I- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY  
 CC -I- (MYOTROPIC ACTIVITY).  
 CC -I- SIMILARITY: BELONGS TO THE KININ FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 8  
 SQ SEQUENCE 8 AA; 839 MW; 736365A5B9D6DD8 CRC64;

Query Match 24.7%; Score 22; DB 5; Length 8;  
 Best Local Similarity 75.0%; Pred. No. 6.7e+05;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 NSWG 5  
 DB 5 SSWG 8

## RESULT 21

ID 077914 PRELIMINARY; PRT; 11 AA.  
 AC 077914;  
 DT 01-NOV-1998 (TREMblrel. 08, Created)  
 DT 01-NOV-1998 (TREMblrel. 08, last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, last annotation update)  
 DE MHC class II B locus 9 (Fragment).  
 OS Oreochromis niloticus (Nile tilapia).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Labroidel;  
 OC Cichlidae; Oreochromis.  
 OX NCBI\_Taxid=8128;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=98315113; PubMed=9649539;  
 RA Malaga-Tillio E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,  
 RA Figueroa F., Sultmann H., Klein J.;  
 RT "Linkage relationships and haplotype polymorphism among cichlid mhc  
 RT class II B loci.";  
 RL Genetics 149:1527-1537(1998).

DR EMBL: AF050025; AAC41364.1; -  
 FT NON\_TER 1  
 SQ SEQUENCE 11 AA; 1167 MW; 2F46D347A2C045A3 CRC64;

Query Match  
 Best Local Similarity 24.7%; Score 22; DB 7; Length 11;  
 Matches 4; Conservative 3; Mismatches 1; Indels 4; Gaps 1;

OY 1 LNSMCKGRITC 12  
 :||| :||  
 Db 1 MDSMS----IVC 8

## RESULT 22

O56947 PRELIMINARY; PRT; 12 AA.

AC O56947;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DE Hypothetical 1.6 kDa protein (Fragment).  
 OS Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Yersinia.  
 NCBI\_TaxID=633;  
 RX MEDLINE=96125720; PubMed=8541300;  
 RA Hobbs M., Reeves P.R.;  
 RT "Genetic organization and evolution of Yersinia pseudotuberculosis  
 3.6-dideoxyhexose biosynthetic genes";  
 RL Biochim. Biophys. Acta 1245:273-277(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=GROUP IA;  
 RA Reeves P.R., Hobbs M., Valvano M.A., Skurnik M., Whitfield C.,  
 RT Coplin D., Kido N., Klena J., Maskell D., Raetz C.R., Rick P.D.;  
 RL Trends Microbiol. 4:495-503(1996).  
 DR EMBL: U29692; AAB48323.1; -  
 KW Hypothetical protein.  
 FT NON\_TER 12  
 SQ SEQUENCE 12 AA; 1563 MW; DB8264F3D433EB9 CRC64;

Query Match  
 Best Local Similarity 24.7%; Score 22; DB 2; Length 12;  
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 6 CKGRIT 11  
 :||| :||  
 Db 6 CKNRYT 11

## RESULT 23

O52920 PRELIMINARY; PRT; 13 AA.

AC O52920;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DE Dctb genes, 5' end (Fragment).  
 OS Rhizobium meliloti (Sinorhizobium meliloti).  
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
 NCBI\_TaxID=387;  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=90152354; PubMed=2695394;  
 RA Wang Y.-P., Birkenhead K., Boesten B., Manian S., O'Gara F.;  
 RT "Genetic analysis and regulation of the Rhizobium meliloti genes

RT controlling C-4-dicarboxylic acid transport.",  
 RL Gene 85:135-144(1989).  
 DR EMBL: M33555; AAA26254.1; -  
 FT NON\_TER 13  
 SQ SEQUENCE 13 AA; 1560 MW; D00F4BE521FEEBD CRC64;

Query Match  
 Best Local Similarity 24.7%; Score 22; DB 2; Length 13;  
 Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 LNSMCK 6  
 :||| :||  
 Db 2 LPDMAC 7

## RESULT 24

O9XLI2 PRELIMINARY; PRT; 13 AA.

AC O9XLI2;  
 DT 01-NOV-1999 (TREMBLrel. 12, Created)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
 DE Cytochrome oxidase I (Fragment).  
 OS Bemisia tabaci (Sweetpotato whitefly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha;  
 OC Aleyrodiformes; Aleyrodidae; Aleyrodinae; Bemisia.  
 NCBI\_TaxID=7038;  
 RX MEDLINE=10583831;  
 RA Frohlich D.R., Torres-Jerez I., Bedford I.D., Markham P.G.,  
 RA Brown J.K.;  
 RT "A phylogeographical analysis of the Bemisia tabaci species complex  
 based on mitochondrial DNA markers".  
 RL Mol. Ecol. 8:1683-1691(1999).  
 DR EMBL: AF110703; AAD28415.1; -  
 KW Mitochondrion.  
 FT NON\_TER 1  
 SQ SEQUENCE 13 AA; 1639 MW; 8DD68729F5744365 CRC64;

Query Match  
 Best Local Similarity 24.7%; Score 22; DB 8; Length 13;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 NSMCK 6  
 :||| :||  
 Db 5 SSWYC 9

## RESULT 25

O69142 PRELIMINARY; PRT; 15 AA.

AC O69142;  
 DT 01-AUG-1998 (TREMBLrel. 07, Created)  
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)  
 DE Protein SIC (Fragment).  
 OS Streptococcus pyogenes.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;  
 OC Streptococcaceae; Streptococcus.  
 NCBI\_TaxID=1314;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=AP1;  
 RX MEDLINE=98298075; PubMed=9632622;  
 RA Berge A., Rasmussen M., Bjorck L.;  
 RT "Identification of an insertion sequence located in a region encoding  
 virulence factors of Streptococcus pyogenes".  
 RL Infect. Immun. 66:3449-3453(1998).  
 DR EMBL: AF064540; AAC38769.1; -

FT NON\_TER 1 1  
SEQUENCE 15 AA; 1552 MW; 87655FEF847401FF CRC64;

Query Match 24.7%; Score 22; DB 2; Length 15;  
Best Local Similarity 44.4%; Pred. No. 4e+03;  
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 6 CKGRICVT 14  
DB 3 CKPSTVPT 11

RESULT 26

O9QVLO PRELIMINARY; PRT; 16 AA.

AC O9QVLO;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE MEPRIN-METALLOENDOPEPTIDASE (Fragment).  
OS Mus sp.  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OC NCBI\_TaxID=10095;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=91363409; PubMed=1888759;  
RA Flannery A.V., Macadam G.C., Beynon R.J.;  
RT "Immunological characterisation of different meprin species in mice."  
RL Biochim. Biophys. Acta 1079:119-122(1991).  
FT NON\_TER 1  
SQ SEQUENCE 16 AA; 1835 MW; 1409706CEADE119A CRC64;

Query Match 24.7%; Score 22; DB 11; Length 16;  
Best Local Similarity 57.1%; Pred. No. 4.3e+03;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 5 GCKGRIT 11  
DB 6 GIKGTVI 12

RESULT 27

O9PRFO PRELIMINARY; PRT; 16 AA.

AC O9PRFO;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)  
DE WNT 5B (Fragment).  
GN WNT5/5B.  
OS Oryzias latipes (Medaka fish).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;  
OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.  
OC NCBI\_TaxID=8090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=DA, AND HNT;  
RX MEDLINE=20082974; PubMed=10613850;  
RA Ohtsuka M., Makino S., Yoda K., Wada H., Naruse K., Mitani H.,  
Shima A., Ozato K., Kimura M., Inoko H.;  
RT "Construction of a linkage map of the Medaka (Oryzias latipes) and  
mapping of the Da mutant locus defective in dorsoventral patterning."  
RL Genome Res. 9:1277-1287(1999).  
DR EMBL; AB030480; BAA85147.1; -;  
DR EMBL; AB030479; BAA85146.1; -;  
FT NON\_TER 1  
SQ SEQUENCE 16 AA; 1802 MW; A7E961E581415DA7 CRC64;

Query Match 24.7%; Score 22; DB 13; Length 16;  
Best Local Similarity 57.1%; Pred. No. 4.3e+03;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 NSWGCKG 8  
DB 9 NSWMSLG 15

RESULT 28

O8VI57 PRELIMINARY; PRT; 17 AA.

AC O8VI57;  
DT 01-MAR-2002 (TREMBLrel. 20, Created)  
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
DE LDLR dan (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OC NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J;  
RA Simon-Chazottes D.C., Tutols S., Bourgade F., Evans M., Kuehn M.,  
Guenet J.-L.;  
RT "Characterization of an insertional mutation responsible for abnormal  
limb development."  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF247636; AAL36969.1; -;  
FT NON\_TER 17  
SQ SEQUENCE 17 AA; 1967 MW; E09EC2E5FFA554AA CRC64;

Query Match 24.7%; Score 22; DB 11; Length 17;  
Best Local Similarity 36.4%; Pred. No. 4.5e+03;  
Matches 4; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

OY 4 WGC-KGRIT 12  
DB 5 WGALLDGLLC 15

RESULT 29

O93TWO PRELIMINARY; PRT; 20 AA.

AC O93TWO;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Pili glycosylation protein PgIC (Fragment).  
GN PgIC.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OC NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NB;  
RX MEDLINE=21246656; PubMed=11349019;  
RA Kahler C.M., Martin L.E., Izeng Y.L., Miller Y.K., Sharkey K.,  
Stephens D.S., Davies J.K.;  
RT "Polymorphisms in Pili glycosylation Locus of Neisseria meningitidis  
Expressing Class II Pili."  
RL Infect. Immun. 69:3597-3604(2001).  
DR EMBL; AF320320; AAK56076.1; -;  
FT NON\_TER 20  
SQ SEQUENCE 20 AA; 2239 MW; 5AAB734AA47D87FB CRC64;

Query Match 24.7%; Score 22; DB 2; Length 20;  
Best Local Similarity 50.0%; Pred. No. 5.3e+03;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 LNSWGC 6  
DB 1 LNSWGC 6

DB 6 LSPWPC 11

RESULT 30

066202 PRELIMINARY; PRT; 12 AA.  
 ID 066202  
 AC 066202; 072765;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Nucleocapsid protein (Fragment).  
 OS Transmissible gastroenteritis virus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;  
 OC Coronaviridae; Coronavirus.  
 OX NCBI\_TaxID=11149;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-PURDUE-115;  
 RX MEDLINE=87224815; PubMed=3035066;  
 RA Laude H., Raschaert D., Huet J.C.;  
 RT "Sequence and N-terminal processing of the transmembrane protein E1 of  
 RL the coronavirus transmissible gastroenteritis virus.";  
 RL J. Gen. Virol. 68:1687-1693(1987).  
 DR EMBL; X05598; CAA29092.1; -  
 KW Nucleocapsid.  
 FT NON\_TER  
 SQ SEQUENCE 12 AA: 1348 MW: 35A1C53F9BD416D8 CRC64;

Query Match 23.6%; Score 21; DB 12; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 4,7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 3 SWG 5  
 Db 9 SWG 11

Search completed: June 5, 2003, 09:00:37  
 Job time : 30 secs

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OM protein - protein search, using sw model

Run on: June 5, 2003, 08:58:39 ; Search time 34 Seconds  
(without alignments)  
58.787 Million cell updates/sec

Title: US-09-605-573a-69\_COPY\_12\_26  
Perfect score: 89  
Sequence: 1 LNSWCKGRICVTS 15

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 289567

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database :

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22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*  
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	86	96.6	16	19	AAW80468
2	86	96.6	17	19	AAW80474
3	81	91.0	16	19	AAW80467
4	77	86.5	16	21	AAW79852
5	77	86.5	20	21	AAW77396
6	75	84.3	16	21	AAW79848
7	75	84.3	16	21	AAW79851
8	74	83.1	16	21	AAW79846
9	72	80.9	15	17	AAW08268
10	72	80.9	15	17	AAW03053

11	72	80.9	15	17	AAW8790	HIV-1 subtype O gp
12	72	80.9	15	19	AAW64405	HIV epitope #8. S
13	72	80.9	15	19	AAW47240	HIV subtype O gp41
14	72	80.9	16	20	AAW82330	HIV-1 subtype O (A
15	72	80.9	16	21	AAW79842	HIV infection dete
16	72	80.9	16	21	AAW79845	HIV infection dete
17	72	80.9	16	21	AAW79847	HIV infection dete
18	72	80.9	16	21	AAW79858	HIV infection dete
19	70	78.7	16	21	AAW79854	HIV infection dete
20	70	78.7	16	21	AAW79857	HIV infection dete
21	69	77.5	16	21	AAW79841	HIV infection dete
22	69	77.5	16	21	AAW79850	HIV infection dete
23	69	77.5	20	18	AAW44680	Happen-peptide con
24	68	76.4	16	21	AAW79849	HIV infection dete
25	68	76.4	17	21	AAW67608	Peptide #8 for det
26	68	76.4	19	18	AAW44681	Happen-peptide con
27	68	76.4	19	18	AAW16381	HIV-1 sub-type B I
28	67	75.3	16	21	AAW79853	HIV infection dete
29	66	74.2	16	21	AAW79844	HIV infection dete
30	65	73.0	16	21	AAW79843	HIV infection dete
31	65	73.0	17	20	AAW05591	HIV-1 group O stra
32	64	71.9	16	21	AAW79856	HIV infection dete
33	64	71.9	17	21	AAW79858	HIV infection dete
34	64	71.9	17	21	AAW67618	Peptide #18 for de
35	63	70.8	16	21	AAW79855	HIV infection dete
36	63	70.8	19	18	AAW16380	HIV-1 sub-type B I
37	62	69.7	18	21	AAW79867	Putative HIV Immun
38	60	67.4	17	21	AAW79829	HIV infection dete
39	59	66.3	19	18	AAW16379	HIV-1 sub-type B I
40	58	65.2	10	20	AAW05593	HIV-1 group O stra
41	58	65.2	18	13	AAW82196	Sequence of synthe
42	58	65.2	19	11	AAW06326	Biologically mem
43	57	64.0	19	16	AAW94578	Synthetic HIV-2 en
44	57	64.0	19	17	AAW04219	HIV-2 gp36 Immunod
45	57	64.0	20	18	AAW35484	HIV peptide from H
46	56	62.9	12	20	AAW05598	HIV-1 group O stra
47	56	62.9	15	20	AAW05592	HIV-1 group O stra
48	56	62.9	17	11	AAW06056	Immunoreactive pep
49	55	61.8	16	19	AAW47242	HIV-1 gp41 derived
50	55	61.8	16	20	AAW82328	HIV-1 subtype F gp
51	55	61.8	16	20	AAW82329	HIV-1 subtype G gp
52	55	61.8	16	23	AAW676500	HIV-1 gp41 antigen
53	55	61.8	17	11	AAW06049	Immunoreactive pep
54	55	61.8	17	11	AAW06057	Immunoreactive pep
55	55	61.8	17	11	AAW06073	Immunoreactive pep
56	55	61.8	17	16	AAW76722	gp-41 epitope from
57	55	61.8	19	17	AAW76722	HIV-1 gp41/2 epit
58	54	60.7	14	16	AAW05594	HIV-1 group O stra
59	54	60.7	14	16	AAW76726	gp32 epitope from
60	54	60.7	14	19	AAW47241	HIV-2 gp33 derive
61	54	60.7	14	21	AAW79820	HIV infection dete
62	54	60.7	14	23	AAW76498	HIV-2 gp36 protein
63	54	60.7	15	17	AAW09341	Cyclic HIV principl
64	54	60.7	16	20	AAW82323	HIV-1 subtype A gp
65	54	60.7	16	20	AAW82324	HIV-1 subtype B gp
66	54	60.7	16	20	AAW82325	HIV-1 subtype C gp
67	54	60.7	17	11	AAW06048	Immunoreactive pep
68	54	60.7	17	11	AAW06071	Immunoreactive pep
69	54	60.7	17	11	AAW06072	Immunoreactive pep
70	54	60.7	17	11	AAW06089	Immunoreactive pep
71	54	60.7	17	17	AAW03340	HIV-2 gp32 epitope
72	54	60.7	18	11	AAW07508	Biologically memom
73	54	60.7	18	23	AAW76499	HIV-2 gp36 protein
74	54	60.7	19	11	AAW05143	Peptide epitope f
75	54	60.7	19	18	AAW44677	Happen-peptide con
76	54	60.7	19	18	AAW16382	HIV-1 sub-type B I
77	54	60.7	20	11	AAW05156	Fusion protein epi
78	54	60.7	20	17	AAW04232	HIV-1 gp41 immunod
79	53	59.6	12	14	AAW41062	HIV-1 gp41 peptide
80	53	59.6	12	17	AAW81557	Mutation #1 of HIV
81	53	59.6	12	17	AAW93063	Mutation #1 of HIV
82	53	59.6	14	11	AAW03967	HIV-antibody react
83	53	59.6	15	9	AAW80178	Sequence of formul

84	53	59.6	15	9	AAp80217	Sequence of crtlc
85	53	59.6	15	20	AAV10339	T cell epitope/MHC
86	53	59.6	16	19	AAW85229	Helper T-cell pept
87	53	59.6	16	20	AAW82343	HIV-1 subtype D gp
88	53	59.6	16	20	AAW82340	HIV-1 subtype D gp
89	53	59.6	17	9	AAp80183	Sequence of forml
90	53	59.6	17	9	AAp81354	Sequence of crtlc
91	53	59.6	17	11	AAW80606	Immunoreactive pep
92	53	59.6	17	11	AAW80605	Immunoreactive pep
93	53	59.6	17	11	AAW80605	Immunoreactive pep
94	53	59.6	17	11	AAW80603	Immunoreactive pep
95	53	59.6	17	11	AAW80604	Immunoreactive pep
96	53	59.6	17	11	AAW80605	Immunoreactive pep
97	53	59.6	17	11	AAW80607	Immunoreactive pep
98	53	59.6	18	12	AAW14442	Biotin-tagged synt
99	53	59.6	19	9	AAW80179	Sequence of forml
100	53	59.6	19	9	AAW80218	Sequence of crtlc

## ALIGNMENTS

## RESULT 1

AAW80468  
ID AAW80468 standard; peptide; 16 AA.

XX  
AC AAW80468;

XX  
DT 28-JAN-1999 (first entry)

XX  
DE Peptide derived from a conserved sequence of group O human HIV.

XX  
KM Group O human immune deficiency virus; HIV; detection; infection.

XX  
OS Synthetic.

OS Immune deficiency virus.

XX  
PN W09845323-A1.

XX  
PD 15-OCT-1998.

XX  
PF 06-APR-1998; 98W0-FR00691.

XX  
PR 24-FEB-1998; 98FR-0002212.

XX  
PR 09-APR-1997; 97FR-0004356.

XX  
PA (SNFI ) PASTEUR SANOFI DIAGNOSTICS SA.

XX  
PI Cheneboux DMB, Delagneau JFH, Gabelle SJX, Rleunier FY;

XX  
DR WPI; 1998-583190/49.

XX  
PT New synthetic peptide(s) - useful for, e.g. detecting infection by

PT human immune deficiency virus of group O

XX  
PS Claim 6; Page 43; 55pp; French.

XX  
CC AAW80459-74 represent synthetic peptides (either linear or cyclised by

CC Cys-Cys disulphide bonds). The peptides represent variable sequences

CC connected around short highly conserved sequences present in isolates

CC of group O human immune deficiency virus (HIV). The peptides are

CC useful as immunological reagents for detecting infection by group O

CC human immune deficiency virus (HIV).

XX  
SQ Sequence 16 AA;

Query Match 96.6%; Score 86; DB 19; Length 16;

Best Local Similarity 86.7%; Pred. No. 2.4e-06;

Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNSWGCKGRIVCYTS 15

DB 2 LNSWGCKGRIVCYTS 16

## RESULT 2

AAW80474  
ID AAW80474 standard; peptide; 17 AA.

XX  
AC AAW80474;

XX  
DT 28-JAN-1999 (first entry)

XX  
DE Peptide derived from a conserved sequence of group O human HIV.

XX  
KM Group O human immune deficiency virus; HIV; detection; infection.

XX  
OS Synthetic.

OS Immune deficiency virus.

XX  
PN W09845323-A1.

XX  
PD 15-OCT-1998.

XX  
PF 06-APR-1998; 98W0-FR00691.

XX  
PR 24-FEB-1998; 98FR-0002212.

XX  
PR 09-APR-1997; 97FR-0004356.

XX  
PA (SNFI ) PASTEUR SANOFI DIAGNOSTICS SA.

XX  
PI Cheneboux DMB, Delagneau JFH, Gabelle SJX, Rleunier FY;

XX  
DR WPI; 1998-583190/49.

XX  
PT New synthetic peptide(s) - useful for, e.g. detecting infection by

PT human immune deficiency virus of group O

XX  
PS Claim 6; Page 45; 55pp; French.

XX  
CC AAW80459-74 represent synthetic peptides (either linear or cyclised by

CC Cys-Cys disulphide bonds). The peptides represent variable sequences

CC connected around short highly conserved sequences present in isolates

CC of group O human immune deficiency virus (HIV). The peptides are

CC useful as immunological reagents for detecting infection by group O

CC human immune deficiency virus (HIV).

XX  
SQ Sequence 17 AA;

Query Match 96.6%; Score 86; DB 19; Length 17;

Best Local Similarity 86.7%; Pred. No. 2.6e-06;

Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNSWGCKGRIVCYTS 15

DB 2 LNSWGCKGRIVCYTS 16

## RESULT 3

AAW80467  
ID AAW80467 standard; peptide; 16 AA.

XX  
AC AAW80467;

XX  
DT 28-JAN-1999 (first entry)

XX  
DE Peptide derived from a conserved sequence of group O human HIV.

XX  
KM Group O human immune deficiency virus; HIV; detection; infection.

XX  
OS Synthetic.

OS Immune deficiency virus.

XX  
PN W09845323-A1.

XX  
PD 15-OCT-1998.

XX 06-APR-1998; 98WO-FR00691.  
XX 24-FEB-1998; 98FR-0002212.  
PR 09-APR-1997; 97FR-0004356.  
XX (SNFI ) PASTEUR SANOFI DIAGNOSTICS SA.  
XX Cheneboux DMB, Delagneau JFH, Gadelle SJX, Rieunier FY;  
XX WPI: 1998-583190/49.  
XX  
XX New synthetic peptide(s) - useful for, e.g., detecting infection by  
XX human immune deficiency virus of group O  
XX  
XX Claim 6; Page 43; 55pp; French.  
XX  
XX AAM80459-74 represent synthetic peptides (either linear or cyclised by  
XX Cys-Cys disulphide bonds). The peptides represent variable sequences  
XX connected around short highly conserved sequences present in isolates  
XX of group O human immune deficiency virus (HIV). The peptides are  
XX useful as immunological reagents for detecting infection by group O  
XX human immune deficiency virus (HIV).  
XX  
XX Sequence 16 AA:  
SQ  
Query Match 91.0%; Score 81; DB 19; Length 16;  
Best Local Similarity 80.0%; Pred. No. 1.4e-05;  
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
OY 1 LNSMGCKGRICVTS 15  
I:|||||I::|||I  
Db 2 LSSMGCKGRICVTS 16  
RESULT 4  
AAV79852  
ID AAV79852 standard; Peptide; 16 AA.  
XX  
XX AAV79852;  
XX  
XX 10-MAY-2000 (first entry)  
XX  
XX HIV infection detection peptide SEQ ID NO:90.  
XX  
XX Varicella zoster virus; HIV; HIV-2; detection; diagnosis; infection;  
XX viral chimeric peptide; therapy; immunological.  
XX  
XX Unidentified.  
XX  
XX WO200001719-A2.  
XX  
XX 13-JAN-2000.  
XX  
XX 02-JUL-1999; 99WO-US15114.  
XX  
XX 02-JUL-1998; 98US-0091659.  
PR 16-OCT-1998; 98US-0104685.  
PR 11-DEC-1998; 98US-0112026.  
XX  
XX (PEPT-) PEPTIDE SOLUTIONS.  
XX  
XX Chowdhury AM, Bernstein D, Kozhich A, Motsenbocker M;  
XX WPI: 2000-171000/15.  
XX  
XX Novel viral-derived peptides used for the detection of human  
XX immunodeficiency virus (HIV) infection, particularly HIV-2 infection  
XX  
XX Disclosure; Fig 1; 67pp; English.  
XX  
XX The present invention describes a peptide (I) for detecting HIV-2  
XX infection, which comprises a core Varicella-zoster protein 51 sequence.  
CC

CC also described in the present invention are methods for detecting HIV  
CC infection. Peptides from the present invention can be used for the  
CC immunological detection of anti-HIV antibody, particularly for HIV-2  
CC testing. The peptides have high sensitivity and selectivity for HIV.  
CC The improved peptides have increased stability which allows the  
CC peptides to react more favourably to give more sensitive tests. AAV79763  
CC to AAV7968 represent peptides used in the exemplification of the  
CC present invention.  
XX  
XX Sequence 16 AA;  
SQ  
Query Match 86.5%; Score 77; DB 21; Length 16;  
Best Local Similarity 73.3%; Pred. No. 5.4e-05;  
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
OY 1 LNSMGCKGRICVTS 15  
I||||I::|||I  
Db 1 LNSMGCKGRICVTS 15  
RESULT 5  
AAV7396  
ID AAV7396 standard; peptide; 20 AA.  
XX  
XX AAV7396;  
XX  
XX 22-MAY-2000 (first entry)  
XX  
XX HIV-1 group O env epitope, SEQ ID NO:112.  
XX  
XX HIV-1 group O; env; gp120; gp41; glycoprotein; monoclonal antibody;  
XX immunosay; positive control; affinity purification; therapeutic;  
XX Escherichia coli; reactive; epitope.  
XX  
XX Human immunodeficiency virus type 1 group O.  
XX Synthetic.  
XX  
XX WO200004383-A2.  
XX  
XX 27-JAN-2000.  
XX  
XX 09-JUL-1999; 99WO-US15469.  
XX  
XX 14-JUL-1998; 98US-0115171.  
XX  
XX (ABBO ) ABBOTT LAB.  
XX  
XX Schaffel JW, Hackett JR, Tyner JD, Hickman RK;  
XX WPI: 2000-171290/15.  
XX  
XX Novel monoclonal antibodies useful as positive control reagent for  
XX detecting human immunodeficiency virus infections and diagnosing,  
XX evaluating or prognosing viral disease  
XX  
XX Claim 20; Page 70; 148pp; English.  
XX  
XX The invention relates to anti-HIV-1 group O monoclonal antibodies, which  
XX may be used as positive control reagents in immunoassays to detect and  
XX differentiate HIV-1 infections. The invention also encompasses a  
XX monoclonal antibody which binds specifically to an HIV-1 group O  
XX antigen, which has no more than 15% cross reactivity to a corresponding  
XX antigen selected from HIV-1 group M antigens and HIV-2 antigens; and a  
XX method of using a monoclonal antibody as a positive control reagent in  
XX an immunoassay for the detection of anti HIV-1 group O antibodies. The  
XX monoclonal antibodies are useful as positive control reagents in  
XX immunoassays capable of detecting anti-HIV-1 group O antibodies. Such  
XX immunoassays involve coupling a monoclonal antibody with HIV group-1  
XX antigen and detecting the antigen-antibody complex. The monoclonal  
XX antibodies of the invention would be used to ensure that the reagents  
XX provided to detect HIV-1 group O antibody were performing properly. The  
XX monoclonal antibodies may also can be immobilised on a matrix and used  
XX for affinity purification of specific HIV-1 group O-derived proteins  
CC

CC from cell cultures or biological tissues. The monoclonal antibodies can  
CC also be used for generating chimeric antibodies for therapeutic use.  
CC different synthetic, recombinant or purified antibodies which identify  
CC different epitopes of HIV antigens can be used in combination in assay to  
CC diagnose, evaluate, or prognosticate HIV disease condition. The  
CC monoclonal antibodies are also useful for differentiating HIV-1 Group O  
CC antigens from HIV-group M and HIV-2 antigens. Sequences AAY77389-Y77398  
CC represent HIV-1 group O env epitopes.

XX  
SQ Sequence 20 AA;

Query Match 86.5%; Score 77; DB 21; Length 20;

Best Local Similarity 85.7%; Pred. No. 6.7e-05; Mismatches 1; Indels 0; Gaps 0;

Db 1 LNSMGCKGRICVT 14  
1 LNSMGCKGRICVT 20

RESULT 6  
AAY79848  
ID AAY79848 standard; Peptide; 16 AA.

XX AAY79848;

XX 10-MAY-2000 (first entry)

DE HIV infection detection peptide SEQ ID NO:86.

XX Varicella zoster virus; HIV; HIV-2; detection; diagnosis; infection;

KW viral chimeric peptide; therapy; immunological.

XX Unidentified.

XX WO200001719-A2.

XX 13-JAN-2000.

XX 02-JUL-1999; 99WO-US15114.

XX 02-JUL-1998; 98US-0091659.

XX 16-OCT-1998; 98US-0104685.

XX 11-DEC-1998; 98US-0112026.

XX (PEPT-) PEPTIDE SOLUTIONS.

XX Chowdhury AM, Bernstein D, Kozhich A, Molsenbocker M;

XX WPI; 2000-171000/15.

XX Novel viral-derived peptides used for the detection of human

XX immunodeficiency virus (HIV) infection, particularly HIV-2 infection

XX Disclosure; Fig 1; 67pp; English.

CC The present invention describes a peptide (I) for detecting HIV-2  
CC infection, which comprises a core Varicella-Zoster protein 51 sequence.  
CC also described in the present invention are methods for detecting HIV  
CC infection. Peptides from the present invention can be used for the  
CC immunological detection of anti-HIV antibody, particularly for HIV-2  
CC testing. The peptides have high sensitivity and selectivity for HIV.  
CC The improved peptides have increased stability which allows the  
CC peptides to react more favourably to give more sensitive tests. AAY79763  
CC to AAY79868 represent peptides used in the exemplification of the  
CC present invention.

XX Sequence 16 AA;

Query Match 84.3%; Score 75; DB 21; Length 16;

Best Local Similarity 80.0%; Pred. No. 0.00011; Mismatches 2; Indels 0; Gaps 0;

QY 1 LNSMGCKGRICVTS 15  
1 LNSMGCKGRICVTS 15

RESULT 7  
AAY79851  
ID AAY79851 standard; Peptide; 16 AA.

XX AAY79851;

XX 10-MAY-2000 (first entry)

DE HIV infection detection peptide SEQ ID NO:89.

XX Varicella zoster virus; HIV; HIV-2; detection; diagnosis; infection;

KW viral chimeric peptide; therapy; immunological.

XX Unidentified.

XX WO200001719-A2.

XX 13-JAN-2000.

XX 02-JUL-1999; 99WO-US15114.

XX 02-JUL-1998; 98US-0091659.

XX 16-OCT-1998; 98US-0104685.

XX 11-DEC-1998; 98US-0112026.

XX (PEPT-) PEPTIDE SOLUTIONS.

XX Chowdhury AM, Bernstein D, Kozhich A, Molsenbocker M;

XX WPI; 2000-171000/15.

XX Novel viral-derived peptides used for the detection of human

XX immunodeficiency virus (HIV) infection, particularly HIV-2 infection

XX Disclosure; Fig 1; 67pp; English.

CC The present invention describes a peptide (I) for detecting HIV-2  
CC infection, which comprises a core Varicella-Zoster protein 51 sequence.  
CC also described in the present invention are methods for detecting HIV  
CC infection. Peptides from the present invention can be used for the  
CC immunological detection of anti-HIV antibody, particularly for HIV-2  
CC testing. The peptides have high sensitivity and selectivity for HIV.  
CC The improved peptides have increased stability which allows the  
CC peptides to react more favourably to give more sensitive tests. AAY79763  
CC to AAY79868 represent peptides used in the exemplification of the  
CC present invention.

XX Sequence 16 AA;

Query Match 84.3%; Score 75; DB 21; Length 16;

Best Local Similarity 80.0%; Pred. No. 0.00011; Mismatches 2; Indels 0; Gaps 0;

QY 1 LNSMGCKGRICVTS 15  
1 LNSMGCKGRICVTS 15

RESULT 8  
AAY79846  
ID AAY79846 standard; Peptide; 16 AA.

XX AAY79846;

XX 10-MAY-2000 (first entry)

DE HIV infection detection peptide SEQ ID NO:84.

XX

KW Varicella zoster virus; HIV; HIV-2; detection; diagnosis; infection;  
 KM viral chimeric peptide; therapy; immunological.  
 XX Unidentified.  
 OS  
 XX WO200001719-A2.  
 PN  
 XX 13-JAN-2000.  
 XX  
 PD 02-JUL-1999; 99WO-US15114.  
 XX  
 PF 02-JUL-1998; 98US-0091659.  
 PR 16-OCT-1998; 98US-0104685.  
 PR 11-DEC-1998; 98US-0112026.  
 XX  
 PA (PEPT-) PEPTIDE SOLUTIONS.  
 PI Chowdhury AM, Bernstein D, Kozhich A, Molsenbocker M;  
 XX WPI: 2000-171000/15.  
 DR  
 XX  
 PS Novel viral-derived peptides used for the detection of human  
 PT immunodeficiency virus (HIV) infection, particularly HIV-2 infection  
 XX  
 PS Disclosure; Fig 1; 67pp; English.  
 CC The present invention describes a peptide (I) for detecting HIV-2  
 CC infection, which comprises a core Varicella-zoster protein 51 sequence.  
 CC also described in the present invention are methods for detecting HIV  
 CC infection. Peptides from the present invention can be used for the  
 CC immunological detection of anti-HIV antibody, particularly for HIV-2  
 CC testing. The peptides have high sensitivity and selectivity for HIV-2  
 CC peptides to react more favourably to give more sensitive tests. AAY9763  
 CC to AAY7968 represent peptides used in the exemplification of the  
 CC present invention.  
 CC  
 SQ Sequence 16 AA;  
 QY  
 Query Match 83.1%; Score 74; DB 21; Length 16;  
 Best Local Similarity 66.7%; Pred. No. 0.00015;  
 Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;  
 Db 1 LNSMCGCKGRICVTS 15  
 1 LNSMCGCKGRICVTS 15  
 1 LNSMCGCKGRICVTS 15  
 RESULT 9  
 AAY08268  
 ID AAY08268 standard; peptide; 15 AA.  
 XX  
 AC AAY08268;  
 XX  
 DT 13-JUL-1999 (first entry)  
 XX  
 DE HIV 1 subtype O gp41 epitope 2.  
 XX  
 KM Epitope: immunological detection; antibody; solid phase; antigen;  
 KM pathogenic organism; bacteria; virus; protozoa; autoimmune antigen;  
 KM seroconversion; sensitivity; gp120; gp41; gp32; NS5; NS4; NS3.  
 XX  
 OS Human immunodeficiency virus type 1.  
 XX  
 PN DE4430972-A1.  
 XX  
 PD 01-FEB-1996.  
 XX  
 PF 31-AUG-1994; 94DE-4430972.  
 XX  
 PR 25-JUL-1994; 94DE-4426276.  
 XX  
 PA (BOEF) BOEHRINGER MANNHEIM GMBH.

XX  
 PI Faatz E, Hoess E, Kruse-Muller C, Offenloch-Hahnle B;  
 PI Seidel C, Wiedmann M, Wienhues-Thelen U;  
 XX  
 DR WPI: 1996-130244/14.  
 XX  
 XX  
 PT Immunassay of specific antibodies using two antigens - one labelled  
 PT and the other bound to solid phase, with at least one having  
 PT multiple epitopes recognised by the antibody to improve sensitivity.  
 XX  
 PS Disclosure; Page 22; 30pp; German.  
 CC This invention describes a method for the immunological detection of  
 CC an antibody which comprises incubating a test sample, in presence of a  
 CC solid phase, with 2 antigens directed against the antibody, one antigen  
 CC (Ag1) carrying a label and the other (Ag2) being either bound to the  
 CC solid phase or bindable to it. The antibody is detected from measurement  
 CC of the label in the solid and/or liquid phases. The new feature is that  
 CC at least one antigen comprises multiple epitope regions reactive with  
 CC antibody. The method is used to detect antibodies related to pathogenic  
 CC organisms (bacteria, viruses or protozoa) or autoimmune antigens,  
 CC especially antibodies against HIV or hepatitis C. The method can detect  
 CC antibodies even very shortly after seroconversion and in cases where new  
 CC microbial subtypes are involved. The use of multiple epitopes improves  
 CC sensitivity (especially for low affinity antibodies) and significantly  
 CC reduces the risk of false negatives from high titre samples caused by  
 CC the hook effect. Multimeric antigens are also more stable than monomeric  
 CC antigens. AAY08261-Y08276 are epitopes used in the method of the  
 CC invention.  
 CC  
 SQ Sequence 15 AA;  
 QY  
 Query Match 80.9%; Score 72; DB 17; Length 15;  
 Best Local Similarity 66.7%; Pred. No. 0.00029;  
 Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;  
 Db 1 LNSMCGCKGRICVTS 15  
 1 LNSMCGCKGRICVTS 15  
 1 LNSMCGCKGRICVTS 15  
 RESULT 10  
 AAY03053  
 ID AAY03053 standard; peptide; 15 AA.  
 XX  
 AC AAY03053;  
 XX  
 DT 20-SEP-1996 (first entry)  
 XX  
 DE Epitope from gp41.  
 XX  
 KM HIV; epitope; hapten-labelled; immunoassay.  
 KM Human immunodeficiency virus type 1, subtype O.  
 XX  
 OS  
 XX  
 PN DE4430973-A1.  
 XX  
 PD 01-FEB-1996.  
 XX  
 PF 31-AUG-1994; 94DE-4430973.  
 XX  
 PR 25-JUL-1994; 94DE-4426276.  
 XX  
 PA (BOEF) BOEHRINGER MANNHEIM GMBH.  
 XX  
 PI Faatz E, Hoess E, Schmitt U, Seidel C, Wienhues-Thelen UH;  
 PI WPI: 1996-130245/14.  
 DR  
 XX  
 XX  
 PT Prepn. of hapten-labelled peptide - by reacting hapten activated  
 PT ester with selected peptide prim. amino gps., useful as reagents for  
 PT detecting specific antibodies.  
 XX



Query Match 80.9%; Score 72; DB 19; Length 15;  
 Best Local Similarity 66.7%; Pred. No. 0.00029;  
 Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 LNSMGCKGRICYS 15  
 I: |||||:|||||  
 Db 1 LSLMGCKGKLVCTYS 15

## RESULT 13

AAW47240  
 ID AAW47240 standard; peptide; 15 AA.  
 XX AAW47240;

AC AAW47240;  
 XX AAW47240;

DT 22-MAY-1998 (first entry)  
 XX

DE HIV subtype 0 gp41 derived immunogenic peptide.  
 XX

KW Immunoglobulin M; IgM; monoclonal antibody; Mab; HIV antigen; gp41;  
 XX immunogenic peptide; immunoassay; HIV seroconversion; detection.

OS Human immunodeficiency virus.  
 XX

Key Location/Qualifiers  
 FH Disulfide-bond 6.12  
 FT  
 XX  
 PN EP810230-A2.  
 XX  
 PD 03-DEC-1997.  
 XX  
 PF 02-JUN-1997; 97EP-010824.  
 XX  
 PR 31-MAY-1996; 96DE-1022088.  
 XX

PA (BOEF ) BOEHRINGER MANNHEIM GMBH.  
 XX  
 PI Borgya A, Faatz E, Huebner-Parajsz C;  
 XX Ofenloch-Haehnle B, Hoeb E;  
 DR WPI: 1998-011012/02.  
 XX  
 PT Monoclonal antibodies against HIV antigens - useful as immunoassay  
 PT controls, etc.  
 XX  
 PS Claim 3; Page 13; 15pp; German.  
 XX  
 CC The present peptide was used in the preparation of an  
 CC immunoglobulin M (IgM) monoclonal antibody (Mab) directed against a  
 CC human immunodeficiency virus (HIV) antigen. The Mab can be used to  
 CC replace serum controls in immunoassays for anti-HIV Ab, the IgM Ab  
 CC being especially useful for early detection of HIV seroconversion.  
 CC The Mab can also be used for quality control in the production of  
 CC HIV antigens for immunoassay kits, as a detection Mab for detecting  
 CC infectious virus particles and as an immunoadsorbents for purifying  
 CC HIV antigens.  
 XX  
 SQ Sequence 15 AA;

Query Match 80.9%; Score 72; DB 19; Length 15;  
 Best Local Similarity 66.7%; Pred. No. 0.00029;  
 Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 LNSMGCKGRICYS 15  
 I: |||||:|||||  
 Db 1 LSLMGCKGKLVCTYS 15

## RESULT 14

AAW82330  
 ID AAW82330 standard; peptide; 16 AA.  
 XX  
 AC AAW82330;

XX 23-FEB-1999 (first entry)  
 DT  
 XX  
 DE HIV-1 subtype O (Ant 70 isolate) gp41 epitope region II peptide.  
 DE  
 XX  
 KW gp41; epitope; antigen; detection; antibody; immunoassay; vaccine.  
 KW  
 XX  
 OS Human immunodeficiency virus type 1.  
 OS  
 XX  
 PN DE19720914-A1.  
 XX  
 PD 19-NOV-1998.  
 XX  
 PF 16-MAY-1997; 97DE-1020914.  
 XX  
 PR 16-MAY-1997; 97DE-1020914.  
 XX  
 PA (BOEF ) BOEHRINGER MANNHEIM GMBH.  
 XX  
 PI Donle F, Faatz E, Hoess E;  
 XX  
 DR WPI: 1999-000526/01.  
 XX  
 PT Immunoassay for human immune deficiency virus antibodies - using  
 PT mixture of antigens from gp41 of sub-types D or E, plus other  
 PT sub-type in group M  
 XX  
 PS Disclosure; Page 4; 12pp; German.  
 XX  
 CC AAW82330 are HIV-1 gp41 epitope region II peptides from various  
 CC HIV-1 subtypes. These antigenic epitopes are used in an immunoassay for  
 CC detecting antibodies against human immune deficiency virus (HIV). The  
 CC method can be used for standard immunoassay formats, particularly  
 CC heterogenous assays and in methods in which HIV antigens and antibodies  
 CC are detected simultaneously. Such antigen fragments are used to raise  
 CC antibodies and in vaccines. These antigen mixtures provide specific and  
 CC unequivocal detection of HIV-1, especially of strains of the widely  
 CC distributed group M, with more reliable results than known methods. Even  
 CC low concentrations of antibodies are detected, so the number of false  
 CC negatives is reduced. Since a mixture of antigens is used, a hook effect  
 CC is less likely to be encountered in samples of high antibody content.  
 XX  
 SQ Sequence 16 AA;

Query Match 80.9%; Score 72; DB 20; Length 16;  
 Best Local Similarity 66.7%; Pred. No. 0.00031;  
 Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 LNSMGCKGRICYS 15  
 I: |||||:|||||  
 Db 1 LSLMGCKGKLVCTYS 15

## RESULT 15

AAV79842  
 ID AAV79842 standard; Peptide; 16 AA.  
 XX  
 AC AAV79842;  
 XX  
 DT 10-MAY-2000 (first entry)  
 XX  
 DE HIV infection detection peptide SEQ ID NO:80.  
 DE  
 XX  
 KW Varicella zoster virus; HIV; HIV-2; detection; diagnosis; infection;  
 KW viral chimeric peptide; therapy; immunological.  
 XX  
 OS Unidentified.  
 OS  
 XX  
 PN WO200001719-A2.  
 XX  
 PD 13-JAN-2000.  
 XX  
 PF 02-JUL-1999; 99WO-US15114.

XX 02-JUL-1998; 98US-0091659.  
PR 16-OCT-1998; 98US-0104685.  
PR 11-DEC-1998; 98US-0112026.  
XX (PEPT-) PEPTIDE SOLUTIONS.  
XX Chowdhury AM, Bernstein D, Kozhich A, Molsenbocker M;  
XX WPI; 2000-171000/15.  
XX Novel viral-derived peptides used for the detection of human  
XX immunodeficiency virus (HIV) infection, particularly HIV-2 infection  
XX disclosure; Fig 1; 67pp; English.  
XX The present invention describes a peptide (1) for detecting HIV-2  
XX infection, which comprises a core Varicella-zoster protein 51 sequence.  
XX also described in the present invention are methods for detecting HIV  
XX infection. Peptides from the present invention can be used for the  
XX immunological detection of anti-HIV antibody, particularly for HIV-2  
XX testing. The peptides have high sensitivity and selectivity for HIV.  
XX The improved peptides have increased stability which allows the  
XX peptides to react more favourably to give more sensitive tests. AAY79763  
XX to AAY79868 represent peptides used in the exemplification of the  
XX present invention.  
XX Sequence 16 AA:  
SQ  
Query Match 80.9%; Score 72; DB 21; Length 16;  
Best Local Similarity 73.3%; Pred. No. 0.00031;  
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
OY 1 LNSWCKGRILICYTS 15  
11:1111111111111111  
DB 1 LNWGCGAGRCVCTYS 15  
RESULT 16  
AAY79845  
ID AAY79845 standard; Peptide; 16 AA.  
XX AAY79845;  
XX 10-MAY-2000 (first entry)  
XX HIV infection detection peptide SEQ ID NO:83.  
XX Varicella zoster virus; HIV; HIV-2; detection; diagnosis; infection;  
XX viral chimeric peptide; therapy; immunological.  
XX unidentified.  
XX WO200001719-A2.  
XX 13-JAN-2000.  
XX 02-JUL-1999; 99WO-US15114.  
XX 02-JUL-1998; 98US-0091659.  
XX 16-OCT-1998; 98US-0104685.  
XX 11-DEC-1998; 98US-0112026.  
XX (PEPT-) PEPTIDE SOLUTIONS.  
XX Chowdhury AM, Bernstein D, Kozhich A, Molsenbocker M;  
XX WPI; 2000-171000/15.  
XX Novel viral-derived peptides used for the detection of human  
XX immunodeficiency virus (HIV) infection, particularly HIV-2 infection  
XX disclosure; Fig 1; 67pp; English.

XX The present invention describes a peptide (1) for detecting HIV-2  
XX infection, which comprises a core Varicella-zoster protein 51 sequence.  
XX also described in the present invention are methods for detecting HIV  
XX infection. Peptides from the present invention can be used for the  
XX immunological detection of anti-HIV antibody, particularly for HIV-2  
XX testing. The peptides have high sensitivity and selectivity for HIV.  
XX The improved peptides have increased stability which allows the  
XX peptides to react more favourably to give more sensitive tests. AAY79763  
XX to AAY79868 represent peptides used in the exemplification of the  
XX present invention.  
XX Sequence 16 AA:  
SQ  
Query Match 80.9%; Score 72; DB 21; Length 16;  
Best Local Similarity 73.3%; Pred. No. 0.00031;  
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
OY 1 LNSWCKGRILICYTS 15  
11:1111111111111111  
DB 1 LNWGCGAGRCVCTYS 15  
RESULT 17  
AAY79847  
ID AAY79847 standard; Peptide; 16 AA.  
XX AAY79847;  
XX 10-MAY-2000 (first entry)  
XX HIV infection detection peptide SEQ ID NO:85.  
XX Varicella zoster virus; HIV; HIV-2; detection; diagnosis; infection;  
XX viral chimeric peptide; therapy; immunological.  
XX unidentified.  
XX WO200001719-A2.  
XX 13-JAN-2000.  
XX 02-JUL-1999; 99WO-US15114.  
XX 02-JUL-1998; 98US-0091659.  
XX 16-OCT-1998; 98US-0104685.  
XX 11-DEC-1998; 98US-0112026.  
XX (PEPT-) PEPTIDE SOLUTIONS.  
XX Chowdhury AM, Bernstein D, Kozhich A, Molsenbocker M;  
XX WPI; 2000-171000/15.  
XX Novel viral-derived peptides used for the detection of human  
XX immunodeficiency virus (HIV) infection, particularly HIV-2 infection  
XX disclosure; Fig 1; 67pp; English.  
XX The present invention describes a peptide (1) for detecting HIV-2  
XX infection, which comprises a core Varicella-zoster protein 51 sequence.  
XX also described in the present invention are methods for detecting HIV  
XX infection. Peptides from the present invention can be used for the  
XX immunological detection of anti-HIV antibody, particularly for HIV-2  
XX testing. The peptides have high sensitivity and selectivity for HIV.  
XX The improved peptides have increased stability which allows the  
XX peptides to react more favourably to give more sensitive tests. AAY79763  
XX to AAY79868 represent peptides used in the exemplification of the  
XX present invention.  
XX Sequence 16 AA:  
SQ  
Query Match 80.9%; Score 72; DB 21; Length 16;



Best Local Similarity 73.3%; Pred. No. 0.00031;  
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 LNSMGCKGRICVTS 15  
DB 1 LNSMGCKGRICVTS 15

## RESULT 18

AAV79858  
ID AAV79858 standard; Peptide: 16 AA.

AC AAV79858;

DT 10-MAY-2000 (first entry)

DE HIV infection detection peptide SEQ ID NO:96.

KW Varicella zoster virus; HIV; HIV-2; detection; diagnosis; infection;  
XX viral chimeric peptide; therapy; immunological.

OS Unidentified.

PN WO200001719-A2.

PD 13-JAN-2000.

PF 02-JUL-1999; 99WO-US15114.

PR 02-JUL-1998; 98US-0091659.

PR 16-OCT-1998; 98US-0104685.

PR 11-DEC-1998; 98US-0112026.

PA (PEPT-) PEPTIDE SOLUTIONS.

PI Chowdhury AM, Bernstein D, Kozhich A, Motsenbocker M;

DR WPI: 2000-171000/15.

PT Novel viral-derived peptides used for the detection of human  
XX immunodeficiency virus (HIV) infection, particularly HIV-2 infection

PS Disclosure; Fig 1; 67pp; English.

XX The present invention describes a peptide (I) for detecting HIV-2  
CC infection, which comprises a core Varicella-zoster protein S1 sequence.  
CC also described in the present invention are methods for detecting HIV  
CC infection. Peptides from the present invention can be used for the  
CC immunological detection of anti-HIV antibody, particularly for HIV-2  
CC testing. The peptides have high sensitivity and selectivity for HIV-2  
CC The improved peptides have increased stability which allows the  
CC peptides to react more favourably to give more sensitive tests.  
CC to AAV79868 represent peptides used in the exemplification of the  
CC present invention. AAV79763

XX Sequence 16 AA;

Query Match 80.9%; Score 72; DB 21; Length 16;  
Best Local Similarity 66.7%; Pred. No. 0.00031;  
Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 LNSMGCKGRICVTS 15  
DB 1 LNSMGCKGRICVTS 15

## RESULT 19

AAV79854  
ID AAV79854 standard; Peptide: 16 AA.

AC AAV79854;

DT 10-MAY-2000 (first entry)

XX HIV infection detection peptide SEQ ID NO:92.

XX Varicella zoster virus; HIV; HIV-2; detection; diagnosis; infection;  
XX viral chimeric peptide; therapy; immunological.

OS Unidentified.

PN WO200001719-A2.

PD 13-JAN-2000.

PF 02-JUL-1999; 99WO-US15114.

PR 02-JUL-1998; 98US-0091659.

PR 16-OCT-1998; 98US-0104685.

PR 11-DEC-1998; 98US-0112026.

PA (PEPT-) PEPTIDE SOLUTIONS.

PI Chowdhury AM, Bernstein D, Kozhich A, Motsenbocker M;

DR WPI: 2000-171000/15.

PT Novel viral-derived peptides used for the detection of human  
XX immunodeficiency virus (HIV) infection, particularly HIV-2 infection

PS Disclosure; Fig 1; 67pp; English.

XX The present invention describes a peptide (I) for detecting HIV-2  
CC infection, which comprises a core Varicella-zoster protein S1 sequence.  
CC also described in the present invention are methods for detecting HIV  
CC infection. Peptides from the present invention can be used for the  
CC immunological detection of anti-HIV antibody, particularly for HIV-2  
CC testing. The peptides have high sensitivity and selectivity for HIV-2  
CC The improved peptides have increased stability which allows the  
CC peptides to react more favourably to give more sensitive tests.  
CC to AAV79868 represent peptides used in the exemplification of the  
CC present invention. AAV79763

XX Sequence 16 AA;

Query Match 78.7%; Score 70; DB 21; Length 16;  
Best Local Similarity 73.3%; Pred. No. 0.00061;  
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 LNSMGCKGRICVTS 15  
DB 1 LNSMGCKGRICVTS 15

## RESULT 20

AAV79857  
ID AAV79857 standard; Peptide: 16 AA.

AC AAV79857;

DT 10-MAY-2000 (first entry)

DE HIV infection detection peptide SEQ ID NO:95.

KW Varicella zoster virus; HIV; HIV-2; detection; diagnosis; infection;  
XX viral chimeric peptide; therapy; immunological.

OS Unidentified.

PN WO200001719-A2.

PD 13-JAN-2000.

PF 02-JUL-1999; 99WO-US15114.

PR 02-JUL-1998; 98US-0091659.



OY 1 LNSWCKGRICYS 15  
 ||||| | : |||||  
 Db 1 LNSWCKANROVCYTS 15

RESULT 23  
 AAW44680

ID AAW44680 standard; peptide: 20 AA.

AC AAW44680;

DT 01-MAY-1998 (first entry)

DE Hapten-peptide conjugate #4 to detect anti-HIV-1 antibodies.

KW Hapten-peptide: HIV; immunoassay; detection; antibody; HIV-1;

OS capture reagent; haptenised peptide; HIV-2.

FT Synthetic.

FT Human immunodeficiency virus type 1.

FT Key Location/Qualifiers

FT Modified-site 1

FT /note- "Alpha amino group of Lys1 is optionally modified

FT by biotin-aminocaproyl"

FT W09641187-A1.

FT 19-DEC-1996.

FT 07-JUN-1996; 96WO-US09507.

FT 07-JUN-1995; 95US-0486657.

FT (ABBO ) ABBOTT LAB.

FT Bridon DP, Chang C, Colpitts TL, Dagfal DJ, Jaffe K;

FT Merchant BR, Sze I;

FT WPI; 1997-108656/10.

FT Immunassay for HIV specific antibody detection - uses peptide

FT haptenised at N terminus for reaction with the initial complex of

FT antibody and capture reagent

PS Claim 1; Page 8; 37pp; English.

CC This sequence represents a peptide derived from the human immuno-

CC deficiency virus-1 (HIV-1) gp41, type 0. N-terminal haptenised peptides

CC AAW44677-82 are used in an improved immunoassay for detecting anti-HIV-1

CC or -2 antibodies (Ab). The method comprises: (1) reacting sample with

CC capture reagent (CR) to form a CR-Ab complex (C); (11) treating this

CC complex with a haptenised peptide conjugate (Cj) to form a C-Cj complex;

CC (111) treating this with an indicator (I) to form a C-Cj-I complex; and

CC (1iv) detecting a signal generated from I. The hapten is attached at a

CC known, predetermined position, outside the epitope so that it cannot

CC interfere with binding to antibody. This provides a better assay than

CC similar peptides haptenised randomly in solution.

SO Sequence 20 AA:

Query Match 77.5%; Score 69; DB 18; Length 20;

Best Local Similarity 71.4%; Pred. No. 0.0011;

Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 LNSWCKGRICYS 14

||:|||||:|||||

Db 7 LSIWCKGKLCICYT 20

RESULT 24

AAV79849

ID AAV79849 standard; peptide: 16 AA.

AC AAV79849;

DT 10-MAY-2000 (first entry)

DE HIV infection detection peptide SEQ ID NO:87.

KW Varicella zoster virus; HIV; HIV-2; detection; diagnosis; infection;

OS viral chimeric peptide; therapy; immunological.

FT Unidentified.

FT W0200001719-A2.

FT 13-JAN-2000.

FT 02-JUL-1999; 99WO-US15114.

FT 02-JUL-1998; 98US-0091659.

FT 16-OCT-1998; 98US-0104685.

FT 11-DEC-1998; 98US-0112026.

FT (PEPT-) PEPTIDE SOLUTIONS.

FT Chowdhury AM, Bernstein D, Kozhich A, Molsenbocker M;

FT WPI; 2000-171000/15.

FT Novel viral-derived peptides used for the detection of human

FT immunodeficiency virus (HIV) infection, particularly HIV-2 infection

FT Disclosure; Fig 1; 67pp; English.

CC The present invention describes a peptide (I) for detecting HIV-2

CC infection, which comprises a core varicella-zoster protein 51 sequence.

CC also described in the present invention are methods for detecting HIV

CC infection. Peptides from the present invention can be used for the

CC immunological detection of anti-HIV antibody, particularly for HIV-2

CC testing. The peptides have high sensitivity and selectivity for HIV.

CC The improved peptides have increased stability which allows the

CC peptides to react more favourably to give more sensitive tests. AAV79763

CC to AAV79868 represent peptides used in the exemplification of the

CC present invention.

SO Sequence 16 AA:

Query Match 76.4%; Score 68; DB 21; Length 16;

Best Local Similarity 73.3%; Pred. No. 0.0012;

Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 LNSWCKGRICYS 15

||||| | : |||||

Db 1 LNSWCKADROVCYTS 15

RESULT 25

AAV67608

ID AAV67608 standard; peptide: 17 AA.

AC AAV67608;

DT 23-MAR-2000 (first entry)

DE Peptide #8 for detecting HIV-1 group O infection.

KW Human immunodeficiency virus-1; HIV-1; gp41 envelope protein; detection;

OS increased structural stability; diagnostic antigen.

FT Synthetic.

FT Key Location/Qualifiers

FT MISC-difference 4



```

FT      /note- "mutated from Ser residue in wild type
FT      Misc-difference 18      sequence (AAW16382)"
FT      /note- "mutated from Thr residue in wild type
FT      sequence (AAW16382)"
XX      WO9640763-A2.
XX      19-DEC-1996.
XX      07-JUN-1996; 96WO-US09655.
XX      07-JUN-1995; 95US-0472597.
XX      (ABBO ) ABBOTT LAB.
XX      Bridon DP, Colplits TL, Daghfal DJ, Jaffe KD, Sze IS,
XX      WPI: 1997-052229/05.
XX      Hybrid polypeptide(s) comprising HIV-1 sub-type B immuno:dominant
XX      region - contg. 1 or more specific amino acid substitutions critical
XX      for detecting HIV-1 sub-type O, useful in immunoassay for detecting
XX      HIV antibodies
XX      Claim 12; Page 25; 34pp: English.
XX      The polypeptides AAW16379-81 represent peptides having point mutations
XX      in the HIV-1 sub-type B immunodominant region (IDR) at positions 604
XX      and/or 610. The peptides correspond to residues 593-611 of the gp41
XX      protein. This peptide has point mutations at positions 604 and 610. The
XX      invention relates to polypeptides which are hybrid polypeptides
XX      comprising the gp41 IDR of HIV-1 sub-type B contg. 1 or more specific
XX      amino acid substitutions critical for the detection of HIV-1 sub-type O.
XX      The polypeptides can be used for the detection of HIV antibodies.
XX      Sequence 19 AA:
SQ
Query Match      76.4%; Score 68; DB 18; Length 19;
Best Local Similarity 71.4%; Pred. No. 0.0014;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
OY      1 LNSWGCKGRICVT 14
        | | | | | | | | | |
        6 LGIMGCKGRICVT 19
DB
RESULT 28
AAV79853
ID      AAV79853 standard; Peptide: 16 AA.
XX
XX      AAV79853;
XX
XX      10-MAY-2000 (first entry)
XX
XX      HIV infection detection peptide SEQ ID NO:91.
XX
XX      Varicella zoster virus; HIV; HIV-2; detection; diagnosis; infection;
XX      viral chimeric peptide; therapy; immunological.
XX
XX      Unidentified.
XX
XX      WO200001719-A2.
XX
XX      13-JAN-2000.
XX
XX      02-JUL-1999; 99WO-US15114.
XX
XX      02-JUL-1998; 98US-0091659.
XX      16-OCT-1998; 98US-0104685.
XX      11-DEC-1998; 98US-0112026.
XX
XX      (PEPT-) PEPTIDE SOLUTIONS.
PA

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XX      Chowdhury AM, Bernstein D, Kozhich A, Molsenbocker M;
XX      WPI: 2000-171000/15.
XX
XX      Novel viral-derived peptides used for the detection of human
XX      immunodeficiency virus (HIV) infection, particularly HIV-2 infection
XX      Disclosure: Fig 1; 67pp: English.
XX
XX      The present invention describes a peptide (I) for detecting HIV-2
XX      infection, which comprises a core Varicella-zoster protein 51 sequence.
XX      also described in the present invention are methods for detecting HIV
XX      infection. Peptides from the present invention can be used for the
XX      immunological detection of anti-HIV antibody, particularly for HIV-2
XX      testing. The peptides have high sensitivity and selectivity for HIV.
XX      The improved peptides have increased stability which allows the
XX      peptides to react more favourably to give more sensitive tests. AAV79763
XX      to AAV79868 represent peptides used in the exemplification of the
XX      present invention.
XX      Sequence 16 AA:
SQ
Query Match      75.3%; Score 67; DB 21; Length 16;
Best Local Similarity 66.7%; Pred. No. 0.0017;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
OY      1 LNSWGCKGRICVTS 15
        | | | | | | | | | |
        1 LNPWGCKGKVCVTS 15
DB
RESULT 29
AAV79844
ID      AAV79844 standard; Peptide: 16 AA.
XX
XX      AAV79844;
XX
XX      10-MAY-2000 (first entry)
XX
XX      HIV infection detection peptide SEQ ID NO:82.
XX
XX      Varicella zoster virus; HIV; HIV-2; detection; diagnosis; infection;
XX      viral chimeric peptide; therapy; immunological.
XX
XX      Unidentified.
XX
XX      WO200001719-A2.
XX
XX      13-JAN-2000.
XX
XX      02-JUL-1999; 99WO-US15114.
XX
XX      02-JUL-1998; 98US-0091659.
XX      16-OCT-1998; 98US-0104685.
XX      11-DEC-1998; 98US-0112026.
XX
XX      (PEPT-) PEPTIDE SOLUTIONS.
XX
XX      Chowdhury AM, Bernstein D, Kozhich A, Molsenbocker M;
XX      WPI: 2000-171000/15.
XX
XX      Novel viral-derived peptides used for the detection of human
XX      immunodeficiency virus (HIV) infection, particularly HIV-2 infection
XX      Disclosure: Fig 1; 67pp: English.
XX
XX      The present invention describes a peptide (I) for detecting HIV-2
XX      infection, which comprises a core Varicella-zoster protein 51 sequence.
XX      also described in the present invention are methods for detecting HIV
XX      infection. Peptides from the present invention can be used for the
XX      immunological detection of anti-HIV antibody, particularly for HIV-2
XX      testing. The peptides have high sensitivity and selectivity for HIV.
XX      The improved peptides have increased stability which allows the
XX      peptides to react more favourably to give more sensitive tests. AAV79763
XX      to AAV79868 represent peptides used in the exemplification of the
XX      present invention.
XX      Sequence 16 AA:
SQ

```

CC testing. The peptides have high sensitivity and selectivity for HIV.  
 CC The improved peptides have increased stability which allows the  
 CC peptides to react more favourably to give more sensitive tests. AAY79763  
 CC to AAY79868 represent peptides used in the exemplification of the  
 CC present invention.

XX  
 SQ Sequence 16 AA;

Query Match 74.2%; Score 66; DB 21; Length 16;  
 Best Local Similarity 66.7%; Pred. No. 0.0024;  
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 LNSMGCKRIICYTS 15  
 ||:|||||:|||||  
 Db 1 LNAMGCANROVCYTS 15

RESULT 30  
 AAY79843  
 ID AAY79843 standard; Peptide; 16 AA.

XX  
 AC AAY79843;

XX  
 DT 10-MAY-2000 (first entry)

XX  
 DE HIV infection detection peptide SEQ ID NO:81.

XX  
 KW Varicella zoster virus; HIV; HIV-2; detection; diagnosis; infection;  
 viral chimeric peptide; therapy; immunological.

XX  
 OS Unidentified.

XX  
 EN WO200001719-A2.

XX  
 PD 13-JAN-2000.

XX  
 PF 02-JUL-1999; 99WO-US15114.

XX  
 PR 02-JUL-1998; 98US-0091659.

XX  
 PR 16-OCT-1998; 98US-0104685.

XX  
 PR 11-DEC-1998; 98US-0112026.

XX  
 PA (PEPT-) PEPTIDE SOLUTIONS.

XX  
 PI Chowdhury AM, Bernstein D, Kozhich A, Molsenbocker M;

XX  
 DR WPI; 2000-171000/15.

XX  
 PT Novel viral-derived peptides used for the detection of human  
 immunodeficiency virus (HIV) infection, particularly HIV-2 infection

XX  
 PS Disclosure; Fig 1; 67pp; English.

XX  
 CC The present invention describes a peptide (I) for detecting HIV-2  
 infection, which comprises a core Varicella-Zoster protein 51 sequence.  
 CC also described in the present invention are methods for detecting HIV  
 CC infection. Peptides from the present invention can be used for the  
 CC immunological detection of anti-HIV antibody, particularly for HIV-2  
 CC testing. The peptides have high sensitivity and selectivity for HIV.  
 CC The improved peptides have increased stability which allows the  
 CC peptides to react more favourably to give more sensitive tests. AAY79763  
 CC to AAY79868 represent peptides used in the exemplification of the  
 CC present invention.

XX  
 SQ Sequence 16 AA;

Query Match 73.0%; Score 65; DB 21; Length 16;  
 Best Local Similarity 66.7%; Pred. No. 0.0034;  
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 LNSMGCKRIICYTS 15  
 ||:|||||:|||||  
 Db 1 LNAMGCANROVCYTS 15

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